



US009169458B2

(12) **United States Patent**  
**Shimazu et al.**

(10) **Patent No.:** **US 9,169,458 B2**  
(45) **Date of Patent:** **Oct. 27, 2015**

(54) **MUTATED ALKALINE CELLULASE**

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(\*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 559 days.

(21) Appl. No.: **13/583,508**

(22) PCT Filed: **Mar. 11, 2011**

(86) PCT No.: **PCT/JP2011/055831**

§ 371 (c)(1),  
(2), (4) Date: **Sep. 7, 2012**

(87) PCT Pub. No.: **WO2011/111836**

PCT Pub. Date: **Sep. 15, 2011**

(65) **Prior Publication Data**

US 2013/0029897 A1 Jan. 31, 2013

(30) **Foreign Application Priority Data**

Mar. 12, 2010	(JP)	2010-056059
Mar. 12, 2010	(JP)	2010-056060
Mar. 18, 2010	(JP)	2010-063212

(51) **Int. Cl.**  
**C12N 9/42** (2006.01)  
**C12N 1/20** (2006.01)  
**C12N 15/00** (2006.01)  
**C07H 21/04** (2006.01)  
**C11D 3/386** (2006.01)

(52) **U.S. Cl.**  
CPC ..... **C11D 3/38645** (2013.01); **C12N 9/2437**  
(2013.01); **C12Y 302/01004** (2013.01)

(58) **Field of Classification Search**  
None  
See application file for complete search history.

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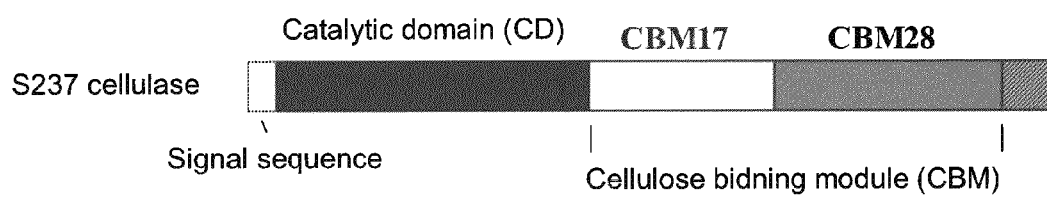
(57) **ABSTRACT**

The present invention provides a mutant alkaline cellulase having enhanced anti-redeposition ability. The present invention provides a mutant alkaline cellulase having an amino acid sequence in which at least amino acid residue selected from the amino acid residues at the positions corresponding to positions 58, 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, 368, 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence of an alkaline cellulase having at least 70% identity with the amino acid sequence of SEQ ID NO: 2, is substituted with other amino acid residue.

**11 Claims, 4 Drawing Sheets**

FIG. 1

A



B

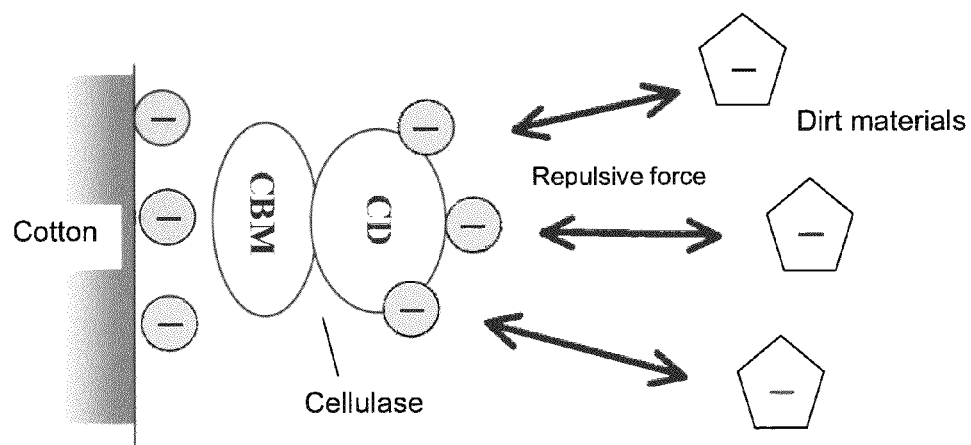
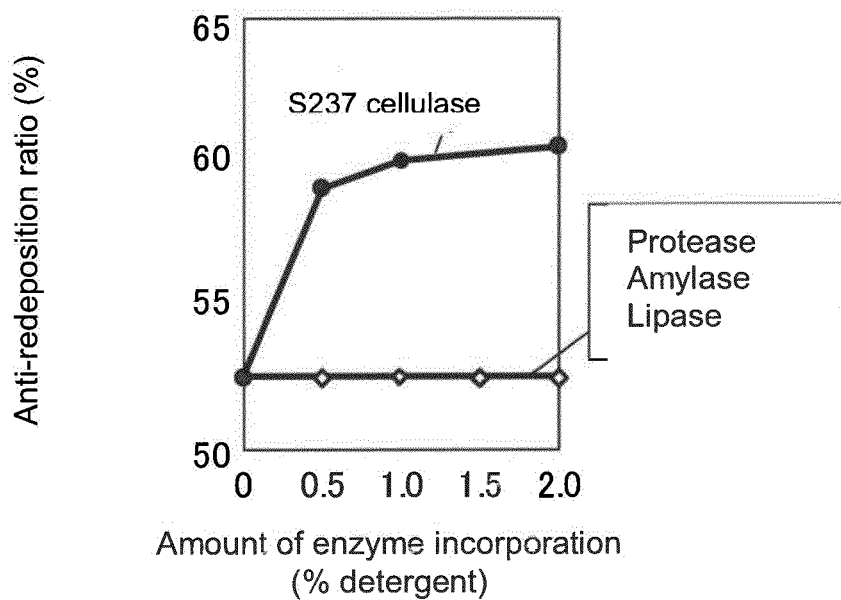


FIG. 2

A



B

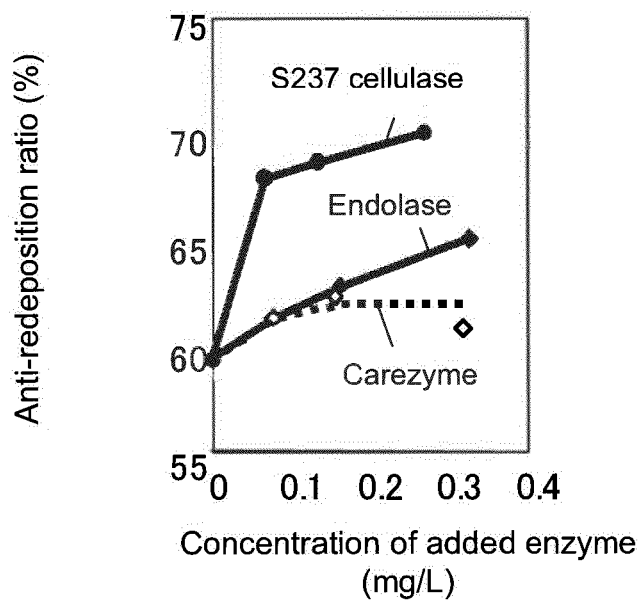


FIG. 3

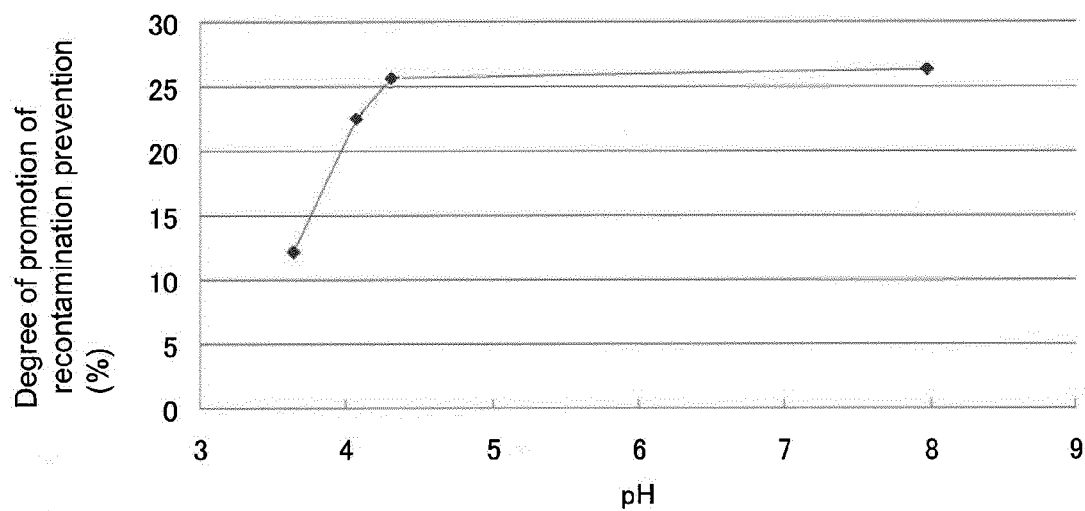
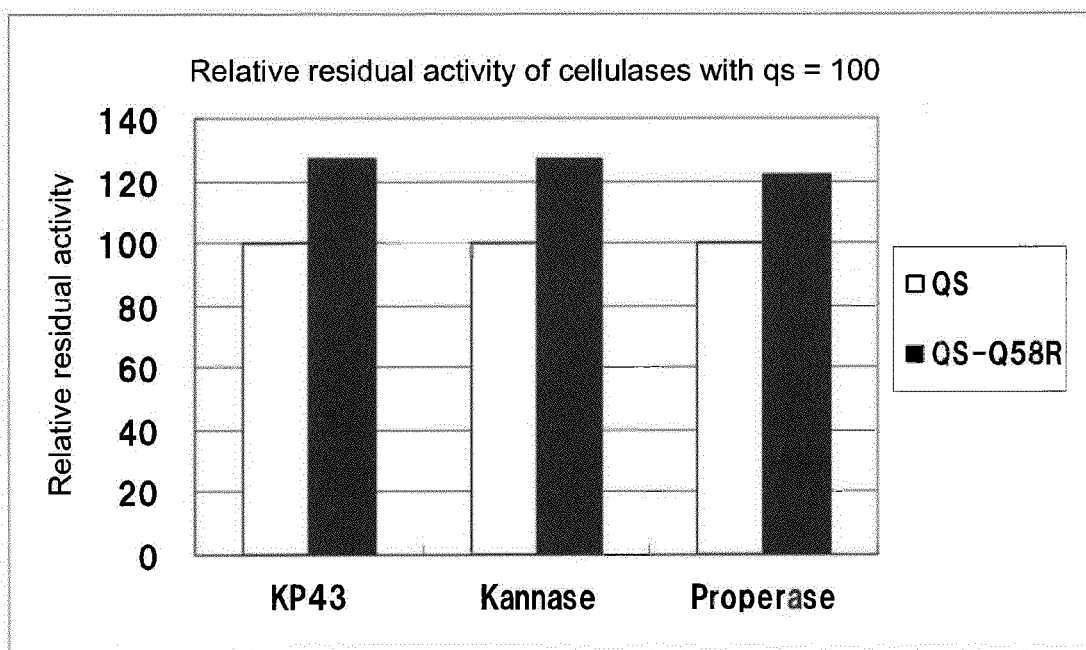


FIG. 4



1

## MUTATED ALKALINE CELLULASE

## FIELD OF THE INVENTION

The present invention relates to a mutant alkaline cellulase having enhanced anti-redeposition ability, and a mutant alkaline cellulase having both enhanced anti-redeposition ability and enhanced protease resistance.

## BACKGROUND OF THE INVENTION

For effective washing of clothing products and the like, it is important to sufficiently detach dirt materials from the object to be washed or to rapidly remove dirt materials through enzymatic degradation or the like, as well as seriously important to prevent reattachment of dirt materials that have been once detached from the object to be washed (preventing of redeposition). Particularly, with regard to minute dirt materials such as soot, it is known that if the dirt materials are once diffused in washing water and then are reattached to the object to be washed, it is very difficult to remove the dirt materials. Accordingly, various anti-redeposition agents have been conventionally incorporated into, for example, detergents for clothing products. Examples of the anti-redeposition agents that may be used include cellulose-based compounds such as carboxymethyl cellulose, hydroxypropylmethyl cellulose, and hydroxybutylmethyl cellulose; nonionic polymers such as polyethylene glycol, polyvinyl alcohol, and polyvinylpyrrolidone; and amino acid polymers. However, there have been needs for development of the anti-redeposition agent having a further enhanced effect.

Meanwhile, it has been a traditional practice to incorporate hydrolases such as proteases, lipases and amylases as cleaning aids, into cleaning agents. Cellulases, which constitute one class of hydrolases, are originally known as enzymes that function in neutral to acidic condition, and it has been conventionally considered that cellulases are not suitable to be incorporated into alkaline cleaning agents for clothing. However, in recent years, alkaline cellulases or variants thereof are obtained from plural organisms including thermophilic or alkalophilic bacteria of the genus *Bacillus*, and the cellulases or variants thereof may also be incorporated into alkaline detergents for clothing (for example, Patent Documents 1 to 6).

Cellulases are enzymes which hydrolyze glycoside bond within  $\beta$ -1,4-glucans including cellulose. Cellulases are mainly produced by bacteria or plants and are available in various kingdoms. Cellulases are classified into endoglucanases (EC3.2.1.4) that degrade cellulose from the interior of the molecule, and exoglucanases (cellobiohydrolases) (EC3.2.1.91) that degrade cellulose from the reduced ends or non-reduced ends of the sugar chain, and release cellobiose. On the other hand, glycoside hydrolases including cellulases are classified into one glycoside hydrolase family, and that family is currently further classified into subfamily 1 to subfamily 108. Cellulases are classified, based on their structures, into families 5, 6, 7, 8, 9, 10, 12, 44, 45, 48, 51, 61, and 74 of the glycoside hydrolase family, and it is also known that the amino acid sequence identity between those families is very low.

However, in recent years, it has been found by analyses of amino acid sequences or three-dimensional structures that cellulases have a common domain having catalytic activity (catalytic domain; CD) and another common functional domain that are linked to each other through a linker. A representative example of the other functional domain is a

2

cellulose binding region having cellulose binding properties (also referred to as cellulose binding module: CBM) (see FIG. 1A). Cellulases usually have plural CBMs. Since cellulose is basically water-insoluble, a cellulase binds to the cellulose surface through the CBMs, and thereby relatively increases the substrate concentration. CBMs are also classified into 40 or more families based on the amino acid sequence identity. In regard to these CBMs, identification of amino acid residues that directly participate in binding to the cellulose has also been carried out (Non-Patent Document 1).

Patent Document 1 discloses a *Bacillus* sp. strain KSM-S237-derived alkaline cellulase having heat resistance, Patent Document 2 discloses a mutant alkaline cellulase having an optimum pH increased to near pH 10.5, and Patent Document 3 discloses a mutant alkaline cellulase having enhanced productivity. Furthermore, Patent Documents 4 and 6 describe that some of these cellulases show anti-redeposition activity.

## PRIOR ART DOCUMENTS

## Patent Document

Patent Document 1: JP-B-3512981  
Patent Document 2: JP-A-2003-310270  
Patent Document 3: JP-A-2004-140  
Patent Document 4: JP-A-2004-536593  
Patent Document 5: JP-A-2006-509850  
Patent Document 6: JP-A-2002-265998

## Non-Patent Document

Non-Patent Document 1: Boraston A. B. et al., *Biochem. J.*, (2002) 361, p. 35-40

## SUMMARY OF THE INVENTION

The present invention includes the following:

[1] A mutant alkaline cellulase having an amino acid sequence in which at least one amino acid residue selected from the amino acid residues at the positions corresponding to positions 58, 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, 368, 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence of an alkaline cellulase having at least 70% identity with the amino acid sequence of SEQ ID NO: 2, is substituted with other amino acid residue.

[2] The mutant alkaline cellulase according to the above item [1], wherein the at last one amino acid residue is a glutamine residue at the position corresponding to position 58 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2.

[3] The mutant alkaline cellulase according to the above item [2], wherein the other amino acid residue is arginine or glutamic acid residue.

[4] The mutant alkaline cellulase according to the above item [1], wherein the at least one amino acid residue is selected from non-charged amino acid residues at the positions corresponding to positions 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175,

3

176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, and 368 of the amino acid sequence set forth in SEQ ID NO: 2, and the other amino acid residue is a charged amino acid residue.

[5] The mutant alkaline cellulase according to the above item [4], wherein the charged amino acid residue is selected from the group consisting of glutamic acid, aspartic acid, lysine, arginine and histidine residue.

[6] The mutant alkaline cellulase according to the above item [4], wherein the non-charged amino acid residue is alanine, serine, glutamine or asparagine residue, and the charged amino acid residue is glutamic acid, aspartic acid or arginine residue.

[7] The mutant alkaline cellulase according to the above item [4], wherein the non-charged amino acid residue is at least one amino acid residue selected from the non-charged amino acid residues at the positions corresponding to positions 71 and 193 of the amino acid sequence set forth in SEQ ID NO: 2, and the charged amino acid residue is an acidic amino acid residue.

[8] The mutant alkaline cellulase according to the above item [1], wherein the at least one amino acid residue is selected from the amino acid residues at the positions corresponding to positions 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence set forth in SEQ ID NO: 2.

[9] The mutant alkaline cellulase according to the above item [8], wherein the at least one amino acid residue is selected from the amino acid residues at the positions corresponding to positions 419, 421, 454, and 501 of the amino acid sequence set forth in SEQ ID NO: 2.

[10] The mutant alkaline cellulase according to the above item [8], wherein the at least one amino acid residue is tryptophan residue while the other amino acid residue is tyrosine residue, or the at least one amino acid residue is an amino acid other than tryptophan residue while the other amino acid residue is alanine residue.

[11] The mutant alkaline cellulase according to the above items [1] to [10], wherein a signal sequence consisting of the amino acid residues at the positions 1 to 30 of the amino acid sequence set forth in SEQ ID NO: 2, or of amino acid residues equivalent to the foregoing amino acid residues, is deleted.

[12] A gene encoding the mutant alkaline cellulase according to any one of the above items [1] to [11].

[13] A recombinant vector including the gene according to the above item [12].

[14] A transformant containing the recombinant vector according to the above item [13].

[15] The transformant according to the above item [14], being a microorganism.

[16] An anti-redeposition agent including the mutant alkaline cellulase according to any one of the above items [1] to [11].

[17] An enzyme composition including the mutant alkaline cellulase according to any one of the above items [1] to [11].

[18] The enzyme composition according to the above item [17], further including one or more enzymes selected from the group consisting of a protease, a cellulase, a  $\beta$ -glucanase, a hemicellulase, a lipase, a peroxidase, a laccase, an  $\alpha$ -amylase, a glucoamylase, a cutinase, a pectinase, a reductase, an oxidase, a phenoloxidase, a ligninase, a pullulanase, a pectate lyase, a xyloglucanase, a xylanase, a pectin acetyltransferase, a polygalacturonase, a rhamnogalacturonase, a pectin lyase,

4

another mannanase, a pectin methylesterase, a cellobiohydrolase, a transglutaminase, and mixtures thereof.

[19] A cleaning agent composition including the mutant alkaline cellulase according to the above items [1] to [11], the anti-redeposition agent according to the above item [16], or the enzyme composition according to the above item [17] or [18].

[20] A method for producing a mutant alkaline cellulase, the method including expressing the mutant alkaline cellulase from the gene according to the above item [12].

[21] A method for enhancing the anti-redeposition ability of an alkaline cellulase, by substituting at least one amino acid residue selected from the amino acid residues at the positions corresponding to positions 58, 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, 368, 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence of an alkaline cellulase having at least 70% identity with the amino acid sequence of SEQ ID NO: 2, with other amino acid residue.

[22] The method according to the above item [21], wherein the at least one amino acid residue is a glutamine residue at the position according to the position 58 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2.

[23] The method according to the above item [21], wherein the at least one amino acid residue is selected from non-charged amino acid residues at the positions corresponding to positions 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, and 368 of the amino acid sequence set forth in SEQ ID NO: 2.

[24] The method according to the above item [21], wherein the at least one amino acid residue is selected from the amino acid residues at the positions corresponding to positions 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence set forth in SEQ ID NO: 2.

[25] A method for enhancing the anti-redeposition ability of an alkaline cellulase, or method for both enhancing the anti-redeposition ability and protease resistance of an alkaline cellulase, wherein a glutamine residue at the position corresponding to position 58 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, is substituted with glutamic acid or arginine.

#### BRIEF DESCRIPTION OF DRAWINGS

FIG. 1 is a schematic diagram of (A) the structure of S237 cellulase, and (B) a speculated mechanism of the effect of preventing redeposition by a cellulase. The signal sequence illustrated in FIG. 1A is usually cut and removed in a mature protein of S237 cellulase.

FIG. 2 is a diagram illustrating the effect for promoting preventing of redeposition provided by the addition of S237 cellulase in comparison with other enzymes. FIG. 2A illustrates the results of comparing S237 cellulase with other hydrolases, and FIG. 2B illustrates the results of comparing S237 cellulase with other cellulases.

FIG. 3 is a diagram illustrating the pH dependency of the anti-redeposition effect provided by the addition of S237 cellulase.

FIG. 4 is a diagram illustrating the results of a comparison of the residual activity (when the activity of S237\_Q242S (QS) is 100) of a cellulase in the presence of various proteases.

## DESCRIPTION OF EMBODIMENTS

The details of the mechanism for prevention of redeposition by cellulases are not clearly known, and in regard to a method for obtaining a cellulase having higher anti-redeposition ability is not yet known. Furthermore, a problem of cellulases being susceptible to degradation by co-existing proteases is known. Thus, further improvement is needed.

The present invention relates to provision of a mutant alkaline cellulase having enhanced anti-redeposition ability, and a mutant alkaline cellulase having enhanced anti-redeposition ability and protease resistance.

The inventors of the present invention conducted a thorough investigation in order to address the problems described above, and as a result, the inventors found that when an amino acid residue at a predetermined position in a *Bacillus* sp. strain KSM-S237-derived alkaline cellulase is substituted with other amino acid residue, the anti-redeposition ability can be enhanced, and in some mutant alkaline cellulases, both anti-redeposition ability and protease resistance can be enhanced.

Furthermore, the inventors of the present invention found that when a non-charged amino acid residue at a predetermined position exposed to the enzyme surface in the catalytic domain of an alkaline cellulase is substituted with a charged amino acid residue so as to increase hydrophilicity of the enzyme surface of the relevant alkaline cellulase, the anti-redeposition ability of the alkaline cellulase can be remarkably enhanced.

Furthermore, the inventors of the present invention found that when an amino acid residue in a region that participates in cellulose binding or the vicinity thereof in the cellulose binding module of an alkaline cellulase is substituted so as to weaken the cellulose binding properties, the anti-redeposition ability of the alkaline cellulase can be further enhanced.

The mutant alkaline cellulase having enhanced anti-redeposition ability according to the present invention, and an anti-redeposition agent containing the mutant alkaline cellulase can bring about a high anti-redeposition promoting effect in, for example, a washing process. The enzyme composition according to the present invention can provide an anti-redeposition effect to a cleaning agent composition and the like when incorporated into the cleaning agent composition and the like. The cleaning agent composition according to the present invention can exhibit a high anti-redeposition effect at the time of washing. When the method for producing a mutant alkaline cellulase according to the present invention is used, production of an alkaline cellulase having enhanced anti-redeposition ability is possible. Furthermore, according to the present invention, an alkaline cellulase which has a high anti-redeposition activity, has both a high anti-redeposition

activity and high protease resistance, and is useful as an enzyme for incorporation into a cleaning agent, can be provided.

Hereinafter, the present invention will be described in detail.

### 1. Mutant Alkaline Cellulase and Production Thereof

In the mutant alkaline cellulase of the present invention, at least one amino acid residue selected from the amino acid residues at the positions corresponding to positions 58, 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, 368, 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence of an alkaline cellulase having at least 70% identity with the amino acid sequence of SEQ ID NO: 2, is substituted with other amino acid residue. The mutant alkaline cellulase of the present invention has enhanced anti-redeposition ability, or has both enhanced anti-redeposition ability and protease resistance, as compared with the alkaline cellulase before mutation (parent alkaline cellulase).

One embodiment of the present invention is a mutant alkaline cellulase which acquires enhanced anti-redeposition ability, or acquires enhanced anti-redeposition ability and protease resistance, by substituting a glutamine residue at the position corresponding to position 58 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence of an alkaline cellulase having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, with other amino acid.

More specifically, the mutant alkaline cellulase of the present invention acquires enhanced anti-redeposition ability, or acquires both enhanced anti-redeposition ability and protease resistance, by substituting a glutamine residue at the position corresponding to position 58 of the amino acid sequence set forth in SEQ ID NO: 2, with glutamic acid or arginine residue.

Another embodiment of the present invention is a mutant alkaline cellulase which acquires enhanced anti-redeposition ability by substituting a non-charged amino acid residue at a particular position in the catalytic domain of any parent alkaline cellulase, with a charged amino acid residue.

More specifically, the mutant alkaline cellulase according to the present invention is a mutant alkaline cellulase obtainable by introducing an amino acid substitution into the amino acid sequence of an available alkaline cellulase, which may be an alkaline cellulase derived from a bacterium of the genus *Bacillus*, such as *Bacillus* sp. strain KSM-S237, or an alkaline cellulase having a high amino acid sequence identity with the foregoing alkaline cellulase, which acquires enhanced anti-redeposition ability by substituting a non-charged amino acid residue that is particularly selected among the non-charged amino acid residues exposed to the enzyme surface in the catalytic domain of the alkaline cellulase with a charged amino acid residue.

Even more specifically, the mutant alkaline cellulase according to the present invention acquires enhanced anti-redeposition ability, by substituting at least one amino acid residue selected from the non-charged amino acid residues at the positions corresponding to positions 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202,



203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, and 368 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of an amino acid of an alkaline cellulase having at least 70% identity with the amino acid sequence of SEQ ID NO: 2, with a charged amino acid residue.

Another embodiment of the present invention is a mutant alkaline cellulase which has enhanced anti-redeposition ability, by substituting an amino acid residue in the region that directly participates in cellulose binding, or a region adjacent thereto, in the cellulose binding module of an available parent alkaline cellulase.

More specifically, the mutant alkaline cellulase according to the present invention is a mutant alkaline cellulase obtainable by introducing an amino acid substitution into the amino acid sequence of an available alkaline cellulase, which may be an alkaline cellulase derived from a bacterium of the genus *Bacillus*, such as *Bacillus* sp. strain KSM-S237, or an alkaline cellulase having high identity of amino acid sequence with that of the foregoing alkaline cellulase, which acquires enhanced anti-redeposition ability by substituting an amino acid residue in the region that directly participates in cellulose binding or a region in the vicinity thereof in the cellulose binding module of the alkaline cellulase, with other amino acid residue.

Even more specifically, the mutant alkaline cellulase according to the present invention acquires enhanced anti-redeposition ability by substituting at least one amino acid residue selected from the amino acid residues at the positions corresponding to positions 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence of an alkaline cellulase having at least 70% identity with the amino acid sequence of SEQ ID NO: 2, with other amino acid residue.

In the present specification, an original alkaline cellulase, that is, an available alkaline cellulase before amino acid substitution, is referred to as a "parent alkaline cellulase", the amino acid sequence thereof is referred to as a "parent amino acid sequence", and the gene encoding the alkaline cellulase is referred to as a "parent alkaline cellulase gene".

The term amino acid residue as used in the present invention means twenty kinds of amino acid residues constituting proteins, namely, Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val.

The term non-charged amino acid as used in the present invention means amino acids that do not have a charge among the twenty kinds of amino acids constituting proteins, that is, non-polar amino acids (valine, alanine, leucine, isoleucine, methionine, phenylalanine, tryptophan, and proline) and polar amino acids (glycine, asparagine, cysteine, glutamine, serine, threonine, and tyrosine). The non-charged amino acid residue that may be subjected to an amino acid substitution in the present invention may be any non-polar amino acid or polar amino acid, and the non-charged amino acid residue is more preferably alanine, serine, glutamine or asparagine.

Furthermore, the term charged amino acid as used in the present invention means amino acids having a charge among the twenty amino acids constituting proteins, that is, acidic amino acids (aspartic acid and glutamic acid), and basic amino acids (arginine, histidine and lysine). The charged amino acid residue that is introduced into the mutant alkaline cellulase by substituting a non-charged amino acid residue in the present invention may be any acidic amino acid or basic

amino acid, and the charged amino acid residue is preferably glutamic acid, aspartic acid or arginine.

According to the present invention, the identity between amino acid sequences refers to the proportion (%) of the number of positions at which amino acid residues are identical between two aligned amino acid sequences, relative to the number of full-length amino acid residues. Specifically, the identity is calculated by the Lipman-Pearson method; Science, 227, 1435 (1985)), and can be computed by performing an analysis using a homology analysis program (Search homology) of the genetic information processing software, Genetyx-Win (Ver. 5.1.1; Software Development, Inc.) by setting the unit size to compare (ktup) at 2.

The amino acid sequence of the mutant alkaline cellulase according to the present invention can be designed by using the amino acid sequence of any available alkaline cellulase as a parent. Examples of such a parent amino acid sequence include the amino acid sequences of the various alkaline cellulases belonging to family 5 of the glycoside hydrolase family. Furthermore, examples of the parent amino acid sequence include the amino acid sequences of alkaline cellulases derived from any available organisms producing alkaline cellulases, such as bacteria of the genus *Bacillus*, bacteria of the genus *Clostridium*, and bacteria of the genus *Acidothermus*. Among these, an amino acid sequence of an alkaline cellulase derived from a bacterium of the genus *Bacillus* can be favorably used.

A suitable example of the alkaline cellulase of a bacterium of the genus *Bacillus* includes *Bacillus* sp. strain KSM-S237-derived alkaline cellulase [S237 cellulase]. The *Bacillus* sp. strain KSM-S237-derived alkaline cellulase, as a precursor protein containing an N-terminal signal sequence (positions 1 to 30 of SEQ ID NO: 2; MMLRKKTKQLISSILIV-LLSLFPAALAA [one-character notation of amino acids]), has the amino acid sequence set forth in SEQ ID NO: 2, and as a mature protein has an amino acid sequence obtained by removing the signal sequence from the amino acid sequence of SEQ ID NO: 2.

Accordingly, examples of the parent amino acid sequence of the mutant alkaline cellulase according to the present invention include the amino acid sequence set forth in SEQ ID NO: 2, as well as amino acid sequences having at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, even more preferably at least 95% identity, even more preferably at least 96% identity, and even more preferably at least 98% identity, with the amino acid sequence set forth in SEQ ID NO: 2. These amino acid sequences may be amino acid sequences encoded in the open reading frame (ORF), or may be amino acid sequences obtained by removing the signal sequence from the foregoing amino acid sequences.

Examples of the alkaline cellulase of a bacterium of the genus *Bacillus* other than S237 cellulase include alkaline cellulases derived from various *Bacillus* bacterial strains, such as *Bacillus* sp. strain DSM12648-derived alkaline cellulase (SEQ ID NO: 4) [the identity of amino acid sequence with that of S237 cellulase (including the signal sequence) is about 98.2%], *Bacillus* sp. strain 1139-derived alkaline cellulase (SEQ ID NO: 6) [the identity of amino acid sequence with that of S237 cellulase (including the signal sequence) is about 91.3%], *Bacillus* sp. strain KSM-64-derived alkaline cellulase (SEQ ID NO: 8) [the identity of amino acid sequence with that of S237 cellulase (including the signal sequence) is about 91.6%], *Bacillus* sp. strain KSM-635-derived alkaline cellulase (SEQ ID NO: 10) [the identity of amino acid sequence with that of S237 cellulase (including the signal sequence) is about 71.0%], and *Bacillus* sp. strain

N-4-derived alkaline cellulase (SEQ ID NO: 12) [the identity of amino acid sequence with that of S237 cellulase (including the signal sequence) is about 64.0%], as well as two kinds of alkaline cellulases such as N131a and N131b derived from *Bacillus* sp. strain KSM-N131 (JP-A No. 2001-231569) [the identity of amino acid sequence with that of S237 cellulase (including the signal sequence) is 87.9% and 97.1%, respectively]. These alkaline cellulases have high mutual amino acid sequence identity and similarity.

Therefore, examples of the parent amino acid sequence of the mutant alkaline cellulase according to the present invention include the amino acid sequences of *Bacillus* sp. strain DSM12648-derived alkaline cellulase (SEQ ID NO: 4), *Bacillus* sp. strain 1139-derived alkaline cellulase (SEQ ID NO: 6), *Bacillus* sp. strain KSM-64-derived alkaline cellulase (SEQ ID NO: 8), *Bacillus* sp. strain KSM-635-derived alkaline cellulase (SEQ ID NO: 10), and *Bacillus* sp. strain N-4-derived alkaline cellulase (SEQ ID NO: 12), as well as amino acid sequences having at least 90% identity, preferably at least 95% identity, more preferably at least 96% identity, and even more preferably at least 98% identity, with the aforementioned amino acid sequences.

Alternatively, when the mutant alkaline cellulase according to the present invention is a variant in which the amino acid residue at the position corresponding to position 58 has been substituted (58<sup>th</sup> position variant), examples of the parent amino acid sequence of the variant include the amino acid sequence of *Bacillus* sp. strain KSM-S237-derived alkaline cellulase as set forth in SEQ ID NO: 2, as well as amino acid sequences having at least 90% identity, more preferably at least 95% identity, even more preferably at least 96% identity, and even more preferably at least 98% identity, with the amino acid sequence set forth in SEQ ID NO: 2.

Examples of a parent alkaline cellulase derived from a bacterium of the genus *Bacillus* other than S237 cellulase, which has an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, include the alkaline cellulases having the amino acid sequences set forth in SEQ ID NO: 4, SEQ ID NO: 6 and SEQ ID NO: 8, and the alkaline cellulases derived from various *Bacillus* bacterial strains, such as *Bacillus* sp. strain KSM-N131-derived alkaline cellulase N131b.

The parent amino acid sequence of position 58 variant may be an amino acid sequence encoded in the open reading frame (ORF), or may also be an amino acid sequence having the signal sequence (positions 1 to 30 of SEQ ID NO: 2) removed from the foregoing amino acid sequence.

Furthermore, the parent amino acid sequence according to the present invention may also include amino acid sequences having a deletion, substitution or addition of one or several amino acids with respect to each of the amino acid sequences of SEQ ID NOs: 2, 4, 6, 8, 10 and 12. The "one or several" refers to, hereinafter for example, 1 to 50 amino acids, preferably 1 to 30 amino acids, more preferably 1 to 20 amino acids, even more preferably 1 to 10 amino acids, and even more preferably 1 to 5 amino acids. Examples of such a parent amino acid sequence include, but are not limited to, the amino acid sequences of a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 10 of the amino acid sequence set forth in SEQ ID NO: 2 has been substituted with glutamine, alanine, proline or methionine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 16 has been substituted with asparagine or arginine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 22 has been substituted with proline; a mutant alkaline cellulase in which the amino acid

residue at the position corresponding to position 33 has been substituted with histidine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 39 has been substituted with alanine, threonine or tyrosine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 76 has been substituted with histidine, methionine, valine, threonine or alanine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 109 has been substituted with isoleucine, leucine, serine or valine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 242 has been substituted with alanine, phenylalanine, valine, serine, aspartic acid, glutamic acid, leucine, isoleucine, tyrosine, threonine, methionine or glycine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 263 has been substituted with isoleucine, leucine, proline or valine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 308 has been substituted with alanine, serine, glycine or valine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 462 has been substituted with threonine, leucine, phenylalanine or arginine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 466 has been substituted with leucine, alanine or serine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 468 has been substituted with alanine, aspartic acid, glycine or lysine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 552 has been substituted with methionine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 564 has been substituted with valine, threonine or leucine; a mutant alkaline cellulase in which the amino acid residue at the position corresponding to position 608 has been substituted with isoleucine or arginine; and the mutant alkaline cellulases disclosed in Patent Documents 2 and 3, such as mutant alkaline cellulases having combinations of one or more of the substitutions of amino acid residues described above. Among the amino acid sequences described above, preferred examples include the amino acid sequences of alkaline cellulases having a mutation in which the amino acid residue at position 242 of the amino acid sequence set forth in SEQ ID NO: 2 has been substituted with other amino acid residues. A more preferred example includes the amino acid sequence of an alkaline cellulase having a mutation in which the glutamine residue at position 242 of the amino acid sequence set forth in SEQ ID NO: 2 has been substituted with a serine residue.

According to the present invention, in the parent amino acid sequences such as described above, one or more amino acid residues selected from the amino acid residues at the positions corresponding to positions 58, 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, 368, 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence of an alkaline cellulase having at least 70% identity with the amino acid sequence of SEQ ID NO: 2, can be substituted with other amino acid residues.

According to an exemplary embodiment of the present invention, in the parent amino acid sequences such as

11

described above, the glutamine residue at the position corresponding to position 58 of the amino acid sequence SEQ ID NO: 2 is substituted with other amino acid.

Preferably, the glutamine residue at the position corresponding to position 58 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence of an alkaline cellulase having an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, may be substituted with glutamic acid or arginine residue.

Furthermore, preferably, the mutant alkaline cellulase of the present invention may have an amino acid sequence in which the glutamine residue at the position corresponding to position 58 of the amino acid sequence set forth in SEQ ID NO: 2 in the amino acid sequence of an alkaline cellulase having a substitution of one or several amino acid residues of the amino acid sequence set forth in SEQ ID NO: 2 by other amino acid residues, is substituted with other amino acid residue. For example, the mutant alkaline cellulase of the present invention may have an amino acid sequence in which the glutamine residue at the position corresponding to position 58 of the amino acid sequence set forth in SEQ ID NO: 2 in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of 1 to 20 amino acid residues, preferably 1 to 10 amino acid residues, and more preferably 1 to 5 amino acid residues, by other amino acid residues with respect to the amino acid residues of an alkaline cellulase having the amino acid sequence set forth in SEQ ID NO: 2, is substituted with glutamic acid or arginine residue.

More preferably, the mutant alkaline cellulase of the present invention may have an amino acid sequence in which the glutamine residue at the position corresponding to position 58 of the amino acid sequence set forth in SEQ ID NO: 2 in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of the amino acid residue at position 242 in an alkaline cellulase having the amino acid sequence set forth in SEQ ID NO: 2 by other amino acid residue, is substituted with other amino acid residue.

Even more preferably, the mutant alkaline cellulase of the present invention may have an amino acid sequence in which the glutamine residue at position 58 of the amino acid sequence set forth in SEQ ID NO: 2 in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of the glutamine residue at position 242 of the amino acid sequence set forth in SEQ ID NO: 2 by a serine residue, is substituted with glutamic acid or arginine.

According to another exemplary embodiment of the present invention, in the parent amino acid sequences such as described above, one or more amino acid residues selected from the non-charged amino acid residues at the positions corresponding to positions 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, and 368 of the amino acid sequence set forth in SEQ ID NO: 2, may be subjected to a substitution by charged amino acid residues.

Preferably, one or more amino acid residues selected from the non-charged amino acid residues at the positions corresponding to positions 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, and 368 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence of an alkaline cellulase having at

12

least 70% identity with the amino acid sequence of SEQ ID NO: 2, may be subjected to a substitution by charged amino acid residues.

Furthermore, preferably, the mutant alkaline cellulase of the present invention may have an amino acid sequence in which one or more amino acid residues selected from the non-charged amino acid residues at the positions corresponding to positions 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, and 368 of the amino acid sequence set forth in SEQ ID NO: 2 in the amino acid sequence of a mutant alkaline cellulase having a substitution of one or several amino acid residues by other amino acid residues with respect to an alkaline cellulase having the amino acid sequence set forth in SEQ ID NO: 2, are substituted with charged amino acid residues. For example, the mutant alkaline cellulase of the present invention may have an amino acid sequence in which one or more amino acid residues selected from the non-charged amino acid residues at the positions corresponding to positions 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, and 368 of the amino acid sequence set forth in SEQ ID NO: 2 in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of 1 to 20 amino acid residues, preferably 1 to 10 amino acid residues, and more preferably 1 to 5 amino acid residues, by other amino acids with respect to the amino acid residues of an alkaline cellulase having the amino acid sequence set forth in SEQ ID NO: 2, are substituted with charged amino acid residues.

More preferably, the mutant alkaline cellulase of the present invention may have an amino acid sequence in which one or more amino acid residues selected from the non-charged amino acid residues at the positions corresponding to positions 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, and 368 of the amino acid sequence set forth in SEQ ID NO: 2 in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of the amino acid residue at position 242 in an alkaline cellulase having the amino acid sequence set forth in SEQ ID NO: 2 by other amino acid residue, are substituted with charged amino acid residues.

Even more preferably, the mutant alkaline cellulase of the present invention may have an amino acid sequence in which one or more amino acid residues selected from the non-charged amino acid residues at the positions 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, and 368 of the amino acid sequence set forth in SEQ ID NO: 2 in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of the glutamine residue at position 242 of the amino acid sequence set forth in SEQ ID NO: 2 by a serine residue, are substituted with charged amino acid residues.

According to another exemplary embodiment of the present invention, the amino acid residues in the region that directly participates in cellulose binding or a region adjacent

thereto in the cellulose binding module in a parent amino acid sequence such as described above, are subjected to substitution.

Preferably, one or more of the amino acid residues at the positions corresponding to positions 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of the amino acid sequence of an alkaline cellulase having at least 70% identity with the amino acid sequence of SEQ ID NO: 2, may be subjected to amino acid substitution.

Furthermore, preferably, the mutant alkaline cellulase of the present invention may have an amino acid sequence in which one or more amino acid residues selected from the amino acid residues at the positions corresponding to positions 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence set forth in SEQ ID NO: 2 in the amino acid sequence of a mutant alkaline cellulase having a substitution of one or several amino acid residues by other amino acid residues with respect to the amino acid residues of an alkaline cellulase having the amino acid sequence set forth in SEQ ID NO: 2, are substituted with other amino acid residues. For example, the mutant alkaline cellulase of the present invention may have an amino acid sequence in which one or more amino acid residues selected from the amino acid residues at the positions corresponding to positions 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence set forth in SEQ ID NO: 2 in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of 1 to 20 amino acid residues, preferably 1 to 10 amino acid residues, and more preferably 1 to 5 amino acid residues, by other amino acids with respect to the amino acid residues of an alkaline cellulase having the amino acid sequence set forth in SEQ ID NO: 2, are substituted with other amino acid residues.

More preferably, the mutant alkaline cellulase of the present invention may have an amino acid sequence in which one or more amino acid residues selected from the amino acid residues at the positions corresponding to positions 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence set forth in SEQ ID NO: 2 in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of the amino acid residue at position 242 of the amino acid sequence set forth in SEQ ID NO: 2 by other amino acid residue, are substituted with other amino acid residues.

Even more preferably, the mutant alkaline cellulase of the present invention may have an amino acid sequence in which one or more amino acid residues selected from the amino acid residues at positions 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence set forth in SEQ ID NO: 2 in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of the glutamine residue at position

242 of the amino acid sequence set forth in SEQ ID NO: 2 by a serine residue, are substituted with other amino acid residues.

The phrase "the position corresponding to position "Y" of the amino acid sequence set forth in SEQ ID NO: "X"" is used to assign a predetermined position of amino acid residue in the amino acid sequence of an available alkaline cellulase when the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: "X" (for example, the amino acid sequence of S237 cellulase set forth in SEQ ID NO: 2) is used as a reference sequence. For example, the "amino acid residue at the position corresponding to position "Y" of the amino acid sequence set forth in SEQ ID NO: "X"" means the amino acid residue appearing in the Y-th position counted from the first amino acid residue of the amino acid sequence set forth in SEQ ID NO: "X".

On the other hand, in the case of the amino acid sequence ("Z") of an alkaline cellulase other than SEQ ID NO: "X", the "amino acid residue at the position corresponding to position "Y" of the amino acid sequence set forth in SEQ ID NO: "X"" means the amino acid residue in the amino acid sequence "Z", which is aligned with the Y-th amino acid residue counted from the 1<sup>st</sup> amino acid residue of the amino acid sequence of SEQ ID NO: "X" when the amino acid sequence "Z" is aligned with the amino acid sequence of SEQ ID NO: "X" (that is, aligned in the same column with respect to the alignment). Furthermore, the alignment of the amino acid sequence of SEQ ID NO: "X" and other amino acid sequence may be carried out manually, or the alignment can also be obtained by, for example, using Clustal W multiple alignment program (Thompson, J. D. et al., (1994) *Nucleic Acids Res.* 22, p. 4673-4680) at a default setting. Clustal W can be used at, for example, the websites of European Bioinformatics Institute (EBI, <http://www.ebi.ac.uk/index.html>) or the DNA Data Bank of Japan operated by the National Institute of Genetics in Japan (DDBJ, <http://www.ddbj.nig.ac.jp/Welcome-j.html>).

A person ordinary skilled in the art can further adjust the alignment thus obtained, if necessary, so as to obtain the optimal alignment. It is preferable to determine such an optimal alignment by taking into consideration of the similarity of amino acid sequences or the frequency of the gap that is inserted. Hereinafter, the similarity of amino acid sequences refers to the proportion (%) of the number of positions at which identical or similar amino acid residues are present in both of two amino acid sequences when the amino acid sequences are aligned, relative to the number of full-length amino acid residues. The term similar amino acid residue means an amino acid residue having properties that are similar to each other in terms of polarity or charge and used for so-called conservative substitution, among the twenty kinds of amino acids constituting proteins. Groups composed of such similar amino acid residues are well known to those ordinary skilled in the art, and examples include, but not limited to, arginine and lysine; glutamic acid and aspartic acid; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

When alignment is carried out according to the method described above, the glutamine residue at position 29 in the sequence of SEQ ID NO: 4 (derived from strain DSM12648), the glutamine residue at position 58 in the sequence of SEQ ID NO: 6 (derived from strain 1139), and the glutamine residue at position 57 in the sequence of SEQ ID NO: 8 (derived from strain KSM-64) respectively correspond to the "amino acid residue at the position corresponding to position 58 of the amino acid sequence set forth in SEQ ID NO: 2".

15

Furthermore, as a reference, the amino acid residues respectively corresponding to the positions described above of the sequence of SEQ ID NO: 2 in the respective amino acid sequences of SEQ ID NO: 2 (derived from *Bacillus* sp. strain KSM-S237), SEQ ID NO: 4 (derived from strain DSM12648), SEQ ID NO: 6 (derived from strain 1139), SEQ ID NO: 8 (derived from strain KSM-64), SEQ ID NO: 10 (derived from strain KSM-635), and SEQ ID NO: 12 (derived from strain N-4), which can be used as the parent amino acid sequences, are shown in Table 5 and Table 6 illustrated below.

According to a preferred exemplary embodiment, the mutant alkaline cellulase according to the present invention includes, for example, a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting the glutamine residue at the position corresponding to position 58 of the amino acid sequence of SEQ ID NO: 2 and of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, with glutamic acid or arginine residue; and having an amino acid sequence that is obtained by further removing a signal sequence (corresponding to a sequence including the positions 1 to 30 of SEQ ID NO: 2) from the foregoing sequence. The substitution described above provides remarkably high anti-redeposition ability, or provides both remarkably high anti-redeposition ability and high protease resistance, to the mutant alkaline cellulase.

A preferred example of the mutant alkaline cellulase of the present invention according to this exemplary embodiment includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting the glutamine residue at position 58 of the amino acid sequence set forth in SEQ ID NO: 2 with glutamic acid and arginine; and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence.

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting the glutamine residue at position 58 in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of the glutamine residue at position 242 of the amino acid sequence set forth in SEQ ID NO: 2 by a serine residue, with glutamic acid or arginine residue; and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence.

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting the glutamine residue at position 29 of the amino acid sequence of SEQ ID NO: 4 in the amino acid sequence set forth in SEQ ID NO: 4, with glutamic acid or arginine residue; and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence.

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting the glutamine residue at position 58 of the amino acid sequence of SEQ ID NO: 4 in the amino acid sequence set forth in SEQ ID NO: 6, with glutamic acid or arginine residue; and an amino acid sequence that is obtainable by further removing the signal sequence from the foregoing sequence.

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting the glutamine residue at position 57 of the amino acid sequence of SEQ ID NO: 4 in the amino acid sequence set forth in SEQ ID NO: 8, with glutamic acid or arginine residue; and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence.

16

According to another preferred exemplary embodiment, the mutant alkaline cellulase related to the present invention includes, for example, in a mutant alkaline cellulase having the amino acid sequence set forth in SEQ ID NO: 2 or an amino acid sequence having at least 70% identity with the amino acid sequence of SEQ ID NO: 2, the mutant alkaline cellulase having an amino acid sequence that is obtained by substituting a non-charged amino acid residue at a particular position in the catalytic domain with a charged amino acid residue, and having an amino acid sequence that is obtained by further removing a signal sequence (corresponding to a sequence including the positions 1 to 30 of SEQ ID NO: 2) from the foregoing sequence.

The mutant alkaline cellulase according to the above exemplary embodiment exhibits anti-redeposition ability based on the high hydrophilicity of the enzyme surface and the overall structure of the enzyme. Therefore, in the case of using the mutant alkaline cellulase simply for the purpose of obtaining an anti-redeposition effect, it makes no difference whether the mutant alkaline cellulase has cellulase activity or not. However, from the viewpoint that a glycolytic activity against saccharides including cellulose can also be simultaneously obtained, it is more preferable that the mutant alkaline cellulase related to the present invention has cellulase activity. The relevant mutant alkaline cellulase may have a signal sequence at the N-terminal, or may be in the form of a mature protein having the signal sequence removed therefrom.

In the mutant alkaline cellulase according to the exemplary embodiment described above, the substitution of a non-charged amino acid residue in the catalytic domain with a charged amino acid residue is not limited, and for example, the substitution may be a substitution of alanine, serine, glutamine or asparagine with glutamic acid, aspartic acid or arginine. Such a substitution provides remarkably high anti-redeposition ability to the mutant alkaline cellulase according to the present invention.

A preferred example of the mutant alkaline cellulase in this exemplary embodiment may be a mutant alkaline cellulase in which the non-charged amino acid residue at position 71 in the amino acid sequence set forth in SEQ ID NO: 2 (this is the position of an amino acid residue adjacent to an acidic amino acid) is substituted with an acidic amino acid residue. Such a substitution particularly efficiently increases the hydrophilicity in the vicinity of the substituted amino acid residue, and provides remarkably high anti-redeposition ability to the resulting mutant alkaline cellulase.

Another preferred example may be a mutant alkaline cellulase in which the non-charged amino acid residue of position 71 (this is the position of an amino acid residue adjacent to an acidic amino acid) in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of the glutamine residue at position 242 of the amino acid sequence set forth in SEQ ID NO: 2 by a serine residue, with an acidic amino acid residue. Such a substitution particularly efficiently increases the hydrophilicity in the vicinity of the substituted amino acid residue, and provides remarkably high anti-redeposition ability to the resulting mutant alkaline cellulase.

Another preferred example may be a mutant alkaline cellulase in which the non-charged amino acid residue at position 193 in the amino acid sequence set forth in SEQ ID NO: 2 (this is the position where there is an amino acid residue which is not adjacent to an acidic amino acid) is substituted with a basic amino acid residue. Such substitution particularly efficiently increases the hydrophilicity in the vicinity of

17

the substituted amino acid residue, and provides remarkably high anti-redeposition ability to the resulting mutant alkaline cellulase.

Another preferred example may be a mutant alkaline cellulase in which the non-charged amino acid residue at position 193 (this is the position where there is an amino acid residue which is not adjacent to an acidic amino acid) in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of the glutamine residue at position 242 of the amino acid sequence set forth in SEQ ID NO: 2 with a serine residue, is substituted with a basic amino acid residue. Such a substitution particularly efficiently increases the hydrophilicity in the vicinity of the substituted amino acid residue, and provides remarkably high anti-redeposition ability to the resulting mutant alkaline cellulase.

As another preferred example, the mutant alkaline cellulase according to the present invention includes, for example, a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting one or more amino acid residues selected from the non-charged amino acid residues at the positions corresponding to positions 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, and 368 of the amino acid sequence of SEQ ID NO: 2 and of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, with charged amino acid residues, and having an amino acid sequence that is obtained by further removing a signal sequence (corresponding to a sequence including the positions 1 to 30 of the sequence of SEQ ID NO: 2) from the foregoing sequence.

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting one or more amino acid residues selected from the non-charged amino acid residues at the positions corresponding to positions 16, 23, 27, 31, 35, 37, 42, 74, 90, 93, 94, 95, 96, 98, 101, 111, 132, 135, 146, 147, 149, 150, 152, 164, 165, 166, 167, 168, 170, 173, 174, 188, 196, 198, 199, 222, 238, 243, 247, 248, 251, 253, 268, 281, 283, 289, 295, 316, 325, 327, 328, 331, 334, and 339 of the amino acid sequence of SEQ ID NO: 4 and of the amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 4, with charged amino acid residues, and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence.

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting one or more amino acid residues selected from the non-charged amino acid residues at the positions corresponding to positions 45, 52, 56, 60, 64, 66, 71, 103, 119, 122, 123, 124, 125, 127, 130, 140, 161, 164, 175, 176, 178, 179, 181, 193, 194, 195, 196, 197, 199, 202, 203, 217, 225, 227, 228, 251, 267, 272, 276, 277, 280, 282, 297, 310, 312, 318, 324, 345, 354, 356, 357, 360, 363, and 368 of the amino acid sequence of SEQ ID NO: 6 and of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 6, with charged amino acid residues, and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence.

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting one or more amino acid residues selected from the non-charged amino acid residues at the positions corresponding to positions 44, 51, 55, 59, 63, 65, 70, 102, 118, 121, 122, 123, 124, 126, 129, 139, 160, 163, 174, 175, 177, 178, 180, 192, 193, 194, 195, 196, 198, 201, 202, 216, 224, 226,

18

227, 250, 266, 271, 275, 276, 279, 281, 296, 309, 311, 317, 323, 344, 353, 355, 356, 359, 362, and 367 of the amino acid sequence of SEQ ID NO: 8 and of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 8, with charged amino acid residues, and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence.

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting one or more amino acid residues selected from the non-charged amino acid residues at the positions corresponding to positions 226, 233, 237, 241, 245, 247, 284, 300, 303, 304, 305, 306, 320, 344, 361, 376, 377, 378, 379, 380, 382, 385, 386, 400, 431, 447, 456, 460, 462, 477, 490, 492, 498, 504, 525, 534, 536, 537, and 548 of the amino acid sequence of SEQ ID NO: 10 and of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 10, with charged amino acid residues, and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence.

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting one or more amino acid residues selected from the non-charged amino acid residues at the positions corresponding to positions 63, 71, 75, 79, 83, 85, 90, 122, 138, 142, 143, 144, 146, 193, 207, 208, 210, 222, 223, 224, 225, 226, 228, 231, 232, 246, 254, 256, 257, 281, 297, 302, 306, 310, 348, 354, 375, 384, 386, and 387 of the amino acid sequence of SEQ ID NO: 12 and of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 12, with charged amino acid residues, and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence.

According to an even more preferred exemplary embodiment, the mutant alkaline cellulase according to the present invention includes, for example, a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting the amino acid residues in the region that directly participates in cellulose binding, and a region adjacent thereto, in the cellulose binding module in an alkaline cellulase having the amino acid sequence set forth in SEQ ID NO: 2 and an amino acid sequence having at least 70% identity with the amino acid sequence of SEQ ID NO: 2, with other amino acid residues, and having an amino acid sequence that is obtained by further removing a signal sequence (corresponding to a sequence including the positions 1 to 30 of SEQ ID NO: 2) from the foregoing sequence.

The mutant alkaline cellulase according to this exemplary embodiment exhibits anti-redeposition ability based on a decrease in the cellulose binding properties at the cellulose binding module of the cellulase. Therefore, in the case of using the mutant alkaline cellulase simply for the purpose of obtaining an anti-redeposition effect, it makes no difference whether the mutant alkaline cellulase may have cellulase activity or not. However, from the viewpoint that a glycolytic activity against saccharides including cellulose can also be simultaneously obtained, it is more preferable that the mutant alkaline cellulase related to the present invention have cellulase activity. The mutant alkaline cellulase according to the present invention may have a signal sequence at the N-terminal, or may be in the form of a mature protein having the signal sequence removed therefrom.

In the mutant alkaline cellulase according to the exemplary embodiment described above, the substitution of an amino acid residue as an object by other amino acid residue may be, for example, a substitution of tryptophan (non-polar amino acid) with tyrosine (polar amino acid), or may be a substitut-

tion of an amino acid residue other than tryptophan [that is, as non-polar amino acids, valine, leucine, isoleucine, methionine, phenylalanine and proline; as polar amino acids, glycine, asparagine, cysteine, glutamine, serine, threonine and tyrosine; as acidic amino acids, aspartic acid and glutamic acid; and as basic amino acids, arginine, histidine and lysine] with alanine (non-polar amino acid). Such a substitution provides remarkably high anti-redeposition ability to the mutant alkaline cellulase according to the present invention.

A preferred example of the mutant alkaline cellulase of the present invention in the exemplary embodiment described above is a mutant alkaline cellulase in which one or more amino acid residues selected from the amino acid residues at the positions 419, 421, 454, and 501 of the amino acid sequence set forth in SEQ ID NO: 2 (these are the positions of amino acid residues that directly participate in cellulose binding and their suitable adjacent site (position 640)) are substituted with other amino acid residues. Such a substitution decreases the cellulose binding property in the vicinity of the substituted amino acid residues, and as a result, the substitution brings about a partial decrease in the binding property to cellulose of the resulting mutant alkaline cellulase, while provides remarkably high anti-redeposition ability.

Another preferred example includes a mutant alkaline cellulase in which one or more amino acid residues selected from the amino acid residues at the positions 419, 421, 454 and 501 (these are the positions of amino acid residues that directly participate in cellulose binding and their suitable adjacent site (position 640)) in the amino acid sequence of a mutant alkaline cellulase having a mutation of substitution of the glutamine residue at position 242 of the amino acid sequence set forth in SEQ ID NO: 2 by a serine residue, are substituted with other amino acid residues.

As another preferred example, the mutant alkaline cellulase according to the present invention includes, for example, a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting one or more amino acid residues selected from the amino acid residues at the positions corresponding to positions 418, 419, 420, 421, 422, 453, 454, 455, 457, 458, 459, 494, 495, 496, 500, 501, 502, 503, 504, 550, 551, 552, 604, 605, 606, 607, 608, 640, 641, 642, 644, 645, 646, 683, 684, 685, 690, 691, 692, 693, 694, 739, 740, and 741 of the amino acid sequence of SEQ ID NO: 2 and of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, with other amino acid residues, and having an amino acid sequence that is obtained by further removing a signal sequence (corresponding to a sequence including the positions 1 to 30 of SEQ ID NO: 2) from the foregoing sequence.

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting one or more amino acid residues selected from the amino acid residues at the positions corresponding to positions 389, 390, 391, 392, 393, 424, 425, 426, 428, 429, 430, 465, 466, 467, 471, 472, 473, 474, 475, 521, 522, 523, 523, 575, 576, 577, 578, 579, 611, 612, 613, 615, 616, 617, 654, 655, 656, 661, 662, 664, 665, 710, 711, and 712 of the amino acid sequence of SEQ ID NO: 4 and of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 4, with other amino acid residues, and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence.

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting one or more amino acid residues selected from the amino acid residues at the positions corresponding to positions 418, 419, 420, 421, 422, 452, 453, 454, 456, 457,

458, 493, 494, 495, 499, 500, 501, 502, 503, 548, 549, 550, 602, 603, 604, 605, 606, 638, 639, 640, 642, 643, 644, 681, 682, 683, 688, 689, 690, 691, 692, 737, 738, and 739 of the amino acid sequence of SEQ ID NO: 6 and of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 6, with other amino acid residues, and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence (the strain 1139-derived cellulase contains a signal sequence consisting of 30 amino acids).

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting one or more amino acid residues selected from the amino acid residues at the positions corresponding to positions 417, 418, 419, 420, 421, 451, 452, 453, 455, 456, 457, 492, 493, 494, 498, 499, 500, 501, 502, 547, 548, 549, 601, 602, 603, 604, 605, 637, 638, 639, 641, 642, 643, 680, 681, 682, 687, 688, 689, 690, 691, 736, 737, and 738 of the amino acid sequence of SEQ ID NO: 8 and of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 8, with other amino acid residues, and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence (the strain KSM-64-derived cellulase contains a signal sequence consisting of 29 amino acids).

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting one or more amino acid residues selected from the amino acid residues at the positions corresponding to positions 598, 599, 600, 601, 602, 633, 634, 635, 637, 638, 639, 674, 675, 676, 680, 681, 682, 683, 684, 729, 730, 731, 783, 784, 785, 786, 787, 819, 820, 821, 823, 824, 825, 862, 863, 864, 869, 870, 871, 872, 873, 919, 920, and 921 of the amino acid sequence of SEQ ID NO: 10 and of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 10, with other amino acid residues, and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence (the strain KSM-635-derived cellulase contains a signal sequence consisting of 29 amino acids).

Another preferred example includes a mutant alkaline cellulase having an amino acid sequence that is obtained by substituting one or more amino acid residues selected from the amino acid residues at the positions corresponding to positions 451, 452, 453, 454, 455, 486, 487, 488, 490, 491, 492, 527, 528, 529, 533, 534, 535, 536, 537, 583, 584, 585, 639, 640, 641, 642, 643, 675, 676, 677, 679, 680, 681, 720, 721, 722, 727, 728, 729, 730, 731, 775, 776, and 777 of the amino acid sequence of SEQ ID NO: 12 and of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 12, with other amino acid residues, and having an amino acid sequence that is obtained by further removing the signal sequence from the foregoing sequence (the strain N-4-derived cellulase contains a signal sequence consisting of 28 amino acids).

The mutant alkaline cellulase according to the present invention can be produced by using various technologies for introducing mutation that are known in the pertinent art. For example, the mutant alkaline cellulase according to the present invention can be produced by mutating the nucleotide sequence that encodes an amino acid residue to be substituted in the alkaline cellulase gene that encodes a parent amino acid sequence of the mutant alkaline cellulase (parent alkaline cellulase gene), to a nucleotide sequence that encodes an amino acid residue after substitution, and then expressing the mutant alkaline cellulase from the mutant gene.



The intended introduction of mutation into the parent alkaline cellulase gene can be carried out essentially based on PCR amplification in which the parent alkaline cellulase gene is used as a template DNA, or replication reactions using various DNA polymerases, by using various site-directed mutagenesis methods that are well known to those ordinary skilled in the art. The site-directed mutagenesis method can be carried out by, for example, any technique such as an inverse PCR method or an annealing method (Muramatsu, et al., ed., "New Genetic Engineering Handbook, Revised 4<sup>th</sup> Edition", Yodosha Co., Ltd., p. 82-88). If necessary, various commercially available kits for site-directed mutagenesis, such as QuickChange II Site-Directed Mutagenesis Kit and QuickChange Multi Site-Directed Mutagenesis Kit by Stratagene, Inc. may be used. In the present invention, a method of preparing DNA fragments by respectively amplifying the upstream side and the downstream side of the mutated site by separately using two complementary mutation primers containing the nucleotide mutations to be introduced, and linking the DNA fragments into one by SOE (splicing by overlap extension)-PCR (Horton R. M. et al., Gene (1989) 77(1), p. 61-68) may be used. The procedure for the introduction of mutation using this SOE-PCR method will be described in detail in the Examples described below.

The template DNA containing the parent alkaline cellulase gene can be prepared by extracting the genomic DNA from a organism that produces an alkaline cellulase by a routine method, or by extracting the RNA and synthesizing a cDNA by reverse transcription. As the organism that produces an alkaline cellulase, bacteria including bacteria of the genus *Bacillus*, such as *Bacillus subtilis*, bacteria of the genus *Clostridium* and bacteria of the genus *Acidothermus*, as well as plants and animals have been reported. However, most advanced studies have been conducted on bacteria of the genus *Bacillus*, such as *Bacillus subtilis*, and those organisms are easily available to those ordinary skilled in the art. For example, *Bacillus* sp. strain KSM-S237 (Accession No. FERM BP-7875), strain KSM-64 (Accession No. FERM BP-2886), and strain KSM-635 (Accession No. FERM BP-1485) have been deposited in the International Patent Organism Depository, National Institute of Advanced Industrial Science and Technology (Central 6, 1-1-1, Higashi, Tsukuba-shi, Ibaraki-ken, Japan), under the respective indicated accession numbers.

Preparation of the genomic DNA from these bacterial strains of the genus *Bacillus* can be carried out by using, for example, the method described in Pitcher et al., Lett. Appl. Microbiol., 1989, 8:p. 151-156, or the like. The template DNA containing the parent alkaline cellulase gene may be prepared in the form in which a DNA fragment containing the parent alkaline cellulase gene that has been excised from a prepared cDNA or the genomic DNA, is inserted into an available vector. Meanwhile, previously reported DNA sequences (sequences registered in GenBank) including the base sequences encoding *Bacillus* sp. strain KSM-S237-derived alkaline cellulase (SEQ ID NO: 2), strain DMS12648-derived alkaline cellulase (SEQ ID NO: 4), strain 1139-derived alkaline cellulase (SEQ ID NO: 6), strain KSM-64-derived alkaline cellulase (SEQ ID NO: 8), strain KSM-635-derived alkaline cellulase (SEQ ID NO: 10) and strain N-4-derived alkaline cellulase (SEQ ID NO: 12) are set forth in SEQ ID NO: 1 (GenBank Accession No. AB018420), SEQ ID NO: 3, SEQ ID NO: 5 (GenBank Accession No. D00066), SEQ ID NO: 7 (GenBank Accession No. M84963), SEQ ID NO: 9 (GenBank Accession No. M27420), and SEQ ID NO: 11 (GenBank Accession No. M25500), respectively.

The site-directed mutagenesis into the parent alkaline cellulase gene can be carried out, most generally by using a mutation primer containing the nucleotide mutation to be introduced. Such a mutation primer may be annealed into a region containing the nucleotide sequence encoding the amino acid residues to be subjected in the parent alkaline cellulase gene, and may be designed to include a base sequence having the nucleotide sequence (codon) that encodes the amino acid residue after substitution, instead of the nucleotide sequence (codon) that encodes the amino acid residue to be substituted. The nucleotide sequences (codons) that encode the amino acid residues to be substituted and the amino acid residues after substitution can be appropriately recognized and selected by a person ordinary skilled in the art, based on conventional textbooks and the like.

For example, in the case of substituting the glutamine residue at position 58 of S237 cellulase (SEQ ID NO: 2) with an arginine residue, a primer containing a sequence in which the codon CAA (positions 744 to 746 of SEQ ID NO: 1) corresponding to the glutamine has been changed into the arginine codon GAA (Q58R-FW; SEQ ID NO: 30) and a primer having a complementary sequence thereof (Q58R-RV; SEQ ID NO: 29) can be used as the mutation primers.

Furthermore, for example, in the case of substituting alanine at position 56 of S237 cellulase (SEQ ID NO: 2) with aspartic acid, a primer containing a sequence in which the codon GCA (positions 738 to 740 of SEQ ID NO: 1) corresponding to the alanine has been changed to the aspartic acid codon GAT, 5'-TCTGAGGCTGGCGATTACAAATTA-CAAG-3' (A56D-FW; SEQ ID NO: 33) and a primer having a complementary sequence thereof, 5'-CTTGTAATTGTAAATCGCCAGCCTCAGA-3' (A56D-RV; SEQ ID NO: 34) can be used as the mutation primers.

Furthermore, for example, in the case of substituting asparagine at position 419 of S237 cellulase (SEQ ID NO: 2) with alanine, a primer containing a sequence in which the codon AAT (positions 1827 to 1829 of SEQ ID NO: 1) corresponding to the asparagine has been changed to the alanine codon GCT, 5'-AGGATTGGAGTGGCTTCGGATTCTCCAAA-3' (N419A-FW; SEQ ID NO: 22) and a primer having a complementary sequence thereof (N419A-RV; SEQ ID NO: 21) can be used as the mutation primers.

The primers used in the present invention can be produced by a well known oligonucleotide synthesis method such as a phosphoramidite method (Nucleic Acids Research, 17, 7059-7071, 1989). Such synthesis of primers can be carried out by using, for example, a commercially available oligonucleotide synthesizer (manufactured by Applied Biosystems, Inc. or the like). When site-directed mutagenesis such as described above is carried out by using a primer set including mutation primers and using the parent alkaline cellulase gene as a template DNA, a mutant alkaline cellulase gene having the intended mutation introduced therein can be obtained. The present invention relates also to a mutant alkaline cellulase gene that may be obtained as such. Furthermore, the term "mutant alkaline cellulase gene" as used in the present invention means any nucleic acid fragment (including DNA, mRNA, artificial nucleic acid, and the like) encoding the amino acid sequence of a mutant alkaline cellulase. The "gene" according to the present invention may include other base sequences such as an untranslated region (UTR), in addition to an open reading frame.

A recombinant vector can be produced by inserting the mutant alkaline cellulase gene thus obtained into an available vector by a conventional method, and linking the gene to the vector. There are no particular limitations on the vector used in the present invention, and any vector such as a plasmid, a



phage, a phagemid, a cosmid, a virus, a YAC vector, or a shuttle vector may be used. Such a vector is more preferably, but not limited to, a vector which can be amplified in bacterial cells, particularly bacterial cells of the genus *Bacillus*, and is even more preferably an expression vector capable of inducing the expression of a transgene in the bacterial cells of the genus *Bacillus*. Among others, a shuttle vector, which is a vector capable of replication even in any of organisms other than bacteria of the genus *Bacillus*, can be particularly suitably used in the recombinant production of a mutant alkaline cellulase. Preferred examples of the vector include, but are not limited to, shuttle vectors such as pHY300PLK (an expression vector capable of transforming both *Escherichia coli* and *Bacillus subtilis*; Ishikawa, H. and Shibahara, H., Jpn. J. Genet., (1985) 60, p. 235-243), and pAC<sub>3</sub> (Moriyama, H. et al., Nucleic Acids Res. (1988) 16, p. 8732); plasmids that can be utilized in the transformation of bacteria of the genus *Bacillus*, such as pUB110 (Gryczan, T. J. et al., J. Bacteriol. (1978) 134, p. 318-329), and pTA10607 (Bron, S. et al., Plasmid, 18 (1987), p. 8-15); and secretion vectors capable of adding secretion signals to recombinant proteins (Yamane, et al., "Fusion Protein Produced by *Bacillus subtilis* Secretion Vector", Denpun Kagaku (Starch Science), 34 (1987), p. 163-170). Furthermore, *Escherichia coli*-derived plasmids (for example, pET22b(+), pBR322, pBR325, pUC118, pUC119, pUC18, pUC19, and pBluescript) can also be used.

For the purpose of producing a recombinant mutant alkaline cellulase, the vector is preferably an expression vector. The expression vector may include various elements that are essential to the expression in a host organism (a transcription promoter, a terminator, a ribosome binding site and the like), as well as cis-elements such as a selection marker gene, a polylinker and an enhancer, and useful sequences such as a poly(A) addition signal and a ribosome binding sequence (SD sequence), as necessary.

A transformant can be produced by using a recombinant vector containing the mutant alkaline cellulase gene. In the present invention, when a transformant (transformed cell) is produced by introducing a recombinant vector (specifically, a recombinant expression vector) containing the mutant alkaline cellulase gene according to the present invention into a host cell, and the transformant is cultured under the conditions under which the expression of a recombinant protein is induced, the mutant alkaline cellulase can be produced. The present invention also relates to a transformant produced as such, and a method for producing a mutant alkaline cellulase using the transformant. As the host cell into which a recombinant vector is introduced, microorganisms including bacteria such as *Escherichia coli* and *Bacillus subtilis*, and yeast cells, as well as any cells such as insect cells, animal cells (for example, mammalian cells) and plant cells can be used. According to the present invention, it is particularly preferable to use bacteria of the genus *Bacillus*, such as *Bacillus subtilis*.

Transformation can be carried out by applying well known transformation technologies such as a calcium phosphate method, an electroporation method, a lipofection method, a particle gun method, and a PEG method. Examples of the transformation method applicable to bacteria of the genus *Bacillus* include a competent cell transformation method (Bott, K. F. and Wilson, G. A., J. Bacteriol. (1967) 93, 1925), an electroporation method (Brigidi, P. et al., FEMS Microbiol. Lett. (1990) 55, 135), a protoplast transformation method (Chang, S. and Cohen, S. N., Mol. Gen. Genet., (1979) 168, p. 111-115), and a Tris-PEG method (Takahashi W., et al., J. Bacteriol. (1983) 156, p. 1130-1134).

The transformant for recombinant protein production can be cultured according to methods that are commonly used by those ordinarily skilled in the art. For example, as a medium for culturing a transformant based on a microbial host such as *Escherichia coli* or a yeast cell, any of a natural medium and a synthetic medium may be used as long as it is a medium which contains carbon sources, nitrogen sources, inorganic salts and the like that can be assimilated by the host organism, and can efficiently carry out the culture of the transformant. Ampicillin, tetracyclin and the like may also be added to the medium, in accordance with the type of the drug selection marker. When a microorganism that has been transformed with an expression vector having an inducible promoter is cultured, an inducer may also be added to the medium as necessary. For example, in the case of culturing a bacterium or the like that has been transformed with an expression vector having a Lac promoter, isopropyl-1-thio- $\beta$ -D-galactoside (IPTG) and the like can be added to the medium, and in the case of culturing a bacterium that has been transformed with an expression vector having a trp promoter, indole acetic acid (IAA) and the like can be added to the medium. There are no particular limitations on the culture conditions, and preferably, the culture is carried out under the conditions suitable for the transformed host organism. For example, in the culture of a *Bacillus subtilis* transformant for producing a recombinant protein, for example, LB medium, 2 $\times$ YT medium, 2 $\times$ L-maltose medium, and CSL fermentation medium can be used.

The mutant alkaline cellulase according to the present invention may be expressed from a mutant alkaline cellulase gene or a transcription product thereof, using a cell-free translation system. The "cell-free translation system" is an in vitro transcription/translation system or an in vitro translation system constructed by adding reagents such as amino acids needed for the translation of proteins, to a suspension obtained by mechanically homogenizing the host cells. The mutant alkaline cellulase thus expressed can be acquired from a culture fluid, a cell lysate or a cell-free translation system, by using a general method used for protein purification, for example, centrifugation, ammonium sulfate precipitation, gel chromatography, ion exchange chromatography or affinity chromatography, alone or in appropriate combination. However, a solution such as a culture supernatant or a lysate supernatant separated or concentrated by using centrifugation, an ultrafiltration type filter or the like, can be directly used as a crude enzyme fluid. When the mutant alkaline cellulase thus expressed is not secreted from the cells, the cells may be homogenized, and then separation and purification of the protein may be carried out.

For the mutant alkaline cellulase produced as described above, an enhancement of the anti-redeposition ability can be confirmed by an anti-redeposition ability evaluation method that will be described below.

Furthermore, experiments such as the preparation of the mRNA used in the present invention, production of a cDNA, PCR, RT-PCR, production of a library, ligation into a vector, transformation of cells, determination of the base sequence of DNA, chemical synthesis of nucleic acid, determination of the N-terminal side amino acid sequence of the protein, mutagenesis, and extraction of the protein, can be carried out according to the methods described in conventional manuals for experiment. Examples of such manuals include Molecular Cloning, A laboratory manual (2001) 3<sup>rd</sup> Ed., Sambrook, J. & Russell, D W. Cold Spring Harbor Laboratory Press. Particularly, for the experiment of genetic recombination of *Bacillus subtilis*, for example, reference can be made to general experiment manuals on the genetic manipulation of *Bacillus subtilis*, such as Yoshikawa, Hirofumi, "7.2 *Bacillus subtilis*

## 25

family” “Genetic Research Method II in Lectures on Biochemical Experiment, 2<sup>nd</sup> series”, (1986), Vol. 1, Tokyo Kagakudojin (Tokyo), p. 150-169).

## 2. Evaluation of Properties of Mutant Alkaline Cellulase

### (2-1) Anti-Redeposition Ability

The mutant alkaline cellulase of the present invention shows enhanced anti-redeposition ability as compared with its parent alkaline cellulase.

The “anti-redeposition ability” of the alkaline cellulase (the mutant alkaline cellulase or the parent alkaline cellulase) according to the present invention means the ability of an alkaline cellulase that is incorporated into an aqueous solution, to prevent hydrophobic (oleophilic) dirty materials that are dispersed in the aqueous solution from re-adhering to substrates such as the clothes present in the aqueous solution. Meanwhile, the “anti-redeposition effect” means an effect in which the re-adhering of hydrophobic (oleophilic) dirty materials dispersed in an aqueous solution to substrates such as clothes in the aqueous solution in the presence of an alkaline cellulase (the mutant alkaline cellulase or the parent alkaline cellulase), and the degree of such an effect.

Preferably, the evaluation of the anti-redeposition ability can be carried out by dispersing carbon black as a model for hydrophobic soot stain in water containing a dissolved cleaning agent composition, adding the mutant alkaline cellulase produced as described above to the dispersion liquid to prepare a washing water, washing a white cotton cloth using the washing water, measuring the reflection ratio at 550 nm of the white cloth after washing, and comparing the reflection ratio with the same reflection ratio of an unwashed white cotton cloth. The details of the procedure of the anti-redeposition ability evaluation method are disclosed in the Examples that are described below. Meanwhile, the water used in the anti-redeposition ability evaluation of the present invention can be prepared by appropriately dissolving CaCl<sub>2</sub> and MgCl<sub>2</sub>·6H<sub>2</sub>O in deionized water.

In the anti-redeposition ability evaluation, the anti-redeposition ratio obtained in various test systems can be calculated by the following formula based on the reflection ratio of a white cotton cloth before washing and after washing.

$$\text{Anti-redeposition ratio (\%)} = \left\{ \frac{\text{Reflection ratio of white cotton cloth after test}}{\text{Reflection ratio of white cotton cloth before test}} \right\} \times 100 \quad [\text{Mathematical formula 1}]$$

A value of this redeposition reflection ratio closer to 100% indicates that the amount of redeposition by carbon black is smaller.

Furthermore, the degree of promotion of anti-redeposition (%) as a result of the addition of a mutant alkaline cellulase can be calculated based on the following formula, and on the anti-redeposition ratio calculated for a test system using a washing water to which a mutant alkaline cellulase is added (enzyme-added group) and a test system using a washing water to which a mutant alkaline cellulase is not added (non-enzyme-added group).

$$\text{Degree of promotion of anti-redeposition by enzyme addition (\%)} = \left\{ \frac{\text{Anti-redeposition ratio of enzyme-added group} - \text{Anti-redeposition ratio of non-enzyme-added group}}{\text{Anti-redeposition ratio of non-enzyme-added group}} \right\} \times 100 \quad [\text{Mathematical formula 2}]$$

An increase in this degree of promotion of anti-redeposition (%) indicates that the effect of preventing redeposition by the addition of a mutant alkaline cellulase has greatly improved.

Furthermore, the degree of anti-redeposition ability enhancement (%) for individual mutant alkaline cellulases is

## 26

calculated by the following formula. Further, the “mutant enzyme” in the following formula refers to the mutant alkaline cellulase, and the control enzyme refers to the parent alkaline cellulase, that is, a wild-type alkaline cellulase or an alkaline cellulase before the introduction of mutation.

$$\text{Degree of anti-redeposition ability enhancement (\%)} \text{ for mutant alkaline cellulase} = \left\{ \frac{\text{Anti-redeposition ratio of mutant enzyme-added group} - \text{Anti-redeposition ratio of control enzyme-added group}}{\text{Anti-redeposition ratio of control enzyme-added group}} \right\} \times 100 \quad [\text{Mathematical formula 3}]$$

An increase of this degree of anti-redeposition ability enhancement (%) indicates that the anti-redeposition ability of the mutant alkaline cellulase is greatly improved as compared with before the introduction of mutation.

Although there are no limitations, the mutant alkaline cellulase according to the present invention can exhibit a degree of anti-redeposition ability enhancement (%) of, for example, 1% to 25%, usually 2% to 15%, and more generally 3% to 12.5%.

### (2-2) Cellulose Binding Property

Furthermore, the mutant alkaline cellulase of the present invention can show decreased cellulose binding property as compared with the parent alkaline cellulase.

The decrease of the cellulose binding property in the mutant alkaline cellulase according to the present invention can be confirmed according to a method similar to the anti-redeposition ability evaluation method that will be described below. Specifically, an evaluation cloth (white cotton cloth) is washed in washing water prepared by adding a predetermined amount of an alkaline cellulase, and sodium chloride in an amount of 5% relative to the total amount of the washing water, to water in which a cleaning agent composition is dissolved, using an agitation-type detergency tester at 20° C. After the washing, the white cloth is taken out and lightly wrung out, and is rapidly introduced into 2000 mL of tap water. Subsequently, the white cloth is taken out and dehydrated without rinsing, and is stained with Coomassie Brilliant Blue. The cloth is lightly wrung out and then immersed in a decolorization solution. The cloth is washed with water and is subjected to finish ironing. Subsequently, the brightness (L value) is measured using a spectrophotometer. A control experiment is carried out by the same procedure, except that a wild-type alkaline cellulase is added to the washing water. A comparison is made for the brightness (L value) of the evaluation clothes after washing thus obtained. This L value decreases along with an increase in the amount of proteins adsorbed to the evaluation cloth. Accordingly, as the L value is higher compared to the L value obtained by adding a wild-type alkaline cellulase, it is shown that the amount of the mutant alkaline cellulase adsorbed to the evaluation cloth is reduced, that is, the cellulose binding property is decreased.

### (2-3) Protease Resistance

Furthermore, the mutant alkaline cellulase of the present invention can show enhanced protease resistance as compared with the parent alkaline cellulase.

According to the present invention, the “protease resistance” refers to the stability of the cellulase to protease, which is evaluated by the residual activity of the cellulase in a cleaning agent composition in which various proteases, particularly alkaline proteases, have been incorporated.

Specifically, for example, the protease resistance may be the residual activity (see the following formula) of a cellulase to be evaluated, which is calculated when the cellulase is stored in a cleaning agent composition containing an alkaline protease at 40° C. for 24 hours.

Cellulase residual activity (%)=(Cellulase activity  
after 24 hours of storage/cellulase activity imme-  
diately after preparation)×100 [Mathematical formula 4]

The mutant alkaline cellulase of the present invention exhibits a cellulase residual activity (%) of, for example, 20% to 75%, and usually 50% to 70%, so that the mutant alkaline cellulase exhibits a residual activity enhanced by 15% to 35% as compared with the parent alkaline cellulase.

Therefore, the mutant alkaline cellulase of the present invention having enhanced protease resistance is suitable for use in the co-presence of various proteases. Here, examples of the proteases include commercially available Alcalase, Espersase, Savinase, Everlase, Kannase (registered trademark; Novozymes, Inc.), Properase, Purafect (registered trademark; Genencor, Inc.), and KAP (Kao Corp.).

### 3. Use of Mutant Alkaline Cellulase

The mutant alkaline cellulase according to the present invention shows high anti-redeposition ability towards hydrophobic dirt materials in an aqueous solution. Therefore, the mutant alkaline cellulase according to the present invention can be advantageously used as an anti-redeposition agent. The anti-redeposition agent may contain any additives such as an inert carrier, a pH adjusting agent, a dispersant, a buffering agent and an antiseptic agent, in addition to the mutant alkaline cellulase. When such an anti-redeposition agent is added to an aqueous solution containing an object to be washed, the redeposition of the object to be washed can be favorably prevented. For example, the anti-redeposition agent according to the present invention can be incorporated in detergents such as detergents for clothing and detergents for domestic use, fabric softeners and the like, and used.

The present invention also provides an enzyme composition containing the mutant alkaline cellulase according to the present invention. The enzyme composition according to the present invention means an enzyme preparation containing the mutant alkaline cellulase as an active ingredient. The enzyme composition according to the present invention may further include, in addition to the mutant alkaline cellulase, hydrolases including proteases, cellulases,  $\beta$ -glucanases, hemicellulases, lipases, peroxidases, laccases,  $\alpha$ -amylases, glucoamylases, cutinases, pectinases, reductases, oxidases, phenoloxidases, ligninases, pullulanases, pectate lyases, xyloglucanases, xylanases, pectinacetylsterases, polygalacturonases, rhamnogalacturonases, pectin lyases, other mannanases, pectin methylesterases, cellobiohydrolases, and transglutaminases, as well as mixtures of two or more kinds thereof.

The enzyme composition according to the present invention may also contain other components such as a pH adjusting agent, a buffering agent, an antiseptic, salt, alcohol, sugars, and medium components, in addition to the mutant alkaline cellulase and the other enzymes. The enzyme composition according to the present invention may be in any form such as a powder, granules, or a lyophilized product.

The present invention also provides a cleaning agent composition containing one or more of the mutant alkaline cellulase, anti-redeposition agent, and enzyme composition according to the present invention. The cleaning agent composition according to the present invention may contain known cleaning agent components, for example, a surfactant, a divalent metal ion scavenger, an alkali agent, an anti-redeposition agent, a bleaching agent, a fluorescent agent and the like, in addition to the mutant alkaline cellulase described above, or an anti-redeposition agent and/or enzyme composition containing the mutant alkaline cellulase.

As the surfactant, any surfactants such as anionic surfactants, nonionic surfactants, amphoteric surfactants and cat-

ionic surfactants, can be used singly or in combination of two or more kinds. A more preferred surfactant may be an anionic surfactant or a nonionic surfactant.

Preferred examples of the anionic surfactant include sulfuric acid ester salts of alcohols having 10 to 18 carbon atoms, sulfuric acid ester salts of alkoxylation products of alcohols having 8 to 20 carbon atoms, alkylbenzenesulfonates, alkyl sulfuric acid ester salts, paraffin sulfonates,  $\alpha$ -olefin sulfonates,  $\alpha$ -sulfo fatty acid salts,  $\alpha$ -sulfo fatty acid alkyl ester salts, and fatty acid salts. For example, linear alkylbenzenesulfonates and alkyl sulfates having alkyl chains having 10 to 14 carbon atoms, and more preferably 12 to 14 carbon atoms, can be suitably used as the anionic surfactant in the present invention. As the counter ions of these salts, alkali metal salts or amines are preferred, and particularly, sodium, potassium, monoethanolamine and diethanolamine are preferred.

Preferred examples of the nonionic surfactant include polyoxyalkylene alkyl ( $C_8$ - $C_{20}$ ) ethers, alkyl polyglycosides, polyoxyalkylene alkyl ( $C_8$ - $C_{20}$ ) phenyl ethers, polyoxyalkylene sorbitan fatty acid ( $C_8$ - $C_{22}$ ) esters, polyoxyalkylene glycol fatty acid ( $C_8$ - $C_{22}$ ) esters, and polyoxyethylene polyoxypropylene block polymers. For example, polyoxyethylene (average number of added moles of EO: 6) alkyl ( $C_{12}$ - $C_{14}$ ) ethers can be suitably used as the nonionic surfactant in the present invention.

The total amount of the surfactant in the cleaning agent composition according to the present invention can be appropriately selected by a person having ordinary skill in the art. However, from the viewpoints of detergency and solubility, the total amount of the surfactant is preferably 10 to 60% by mass, more preferably 15 to 50% by mass, and even more preferably 20 to 45% by mass, relative to the mass of the cleaning agent composition. Among others, the content of the anionic surfactant is preferably 1 to 60% by mass, more preferably 1 to 50% by mass, and even more preferably 3 to 40% by mass, relative to the mass of the cleaning agent composition. Furthermore, the content of the nonionic surfactant is preferably 1 to 45% by mass, more preferably 1 to 35% by mass, and even more preferably 4 to 25% by mass, relative to the mass of the cleaning agent composition. The anionic surfactants and the nonionic surfactants can be used singly, and preferably the surfactants are used as mixtures. Further, amphoteric surfactants and cationic surfactants can also be used in combination in accordance with the purpose.

The cleaning agent composition according to the present invention may further include a builder. The builder is a compound which itself has no or only slight detergency, however, when incorporated together with a surfactant, can markedly enhance the detergent ability of the surfactant. Examples of the action of the builder include polyvalent metal cation scavenging action, dirt dispersing action, alkali buffering action, and combinations of two or more kinds thereof. Examples of such a builder include water-soluble inorganic compounds, water-insoluble inorganic compounds, and organic compounds.

Examples of builders as water-soluble inorganic compounds include phosphates (tripolyphosphates, pyrophosphates, metaphosphates, trisodium phosphate, and the like), silicates, carbonates, sulfates, and sulfites. Among them, phosphates are preferred in view of having all of the three types of actions. Examples of builders as water-insoluble inorganic compounds include aluminosilicates (A-type zeolite, P-type zeolite, X-type zeolite, amorphous aluminosilicates, and the like), and crystalline silicates. Examples of builders as organic compounds include carboxylates (aminocarboxylates, hydroxyaminocarboxylates, hydroxycarboxylates, cyclocarboxylates, maleic acid derivatives,

oxalates, and the like), organic carboxylic acid (salt) polymers (acrylic acid polymers and copolymers, polyvalent carboxylic acid (for example, maleic acid and the like) polymers and copolymers, glyoxylic acid polymers, polysaccharides and salts thereof). Among them, organic carboxylic acid (salt) polymers are preferred. With regard to the salt of the builder, alkali metal salts and amines are preferred as the counter ions, and sodium, potassium, monoethanolamine and diethanolamine are more preferred. The builder contained in the cleaning agent composition according to the present invention preferably includes the water-soluble inorganic compounds described above, and is more preferably a combination of the water-soluble inorganic compounds and organic compounds described above. The builder is even more preferably a combination of the water-soluble inorganic compounds, organic compounds and water-insoluble inorganic compounds.

The total amount of the builder in the cleaning agent composition according to the present invention can be appropriately selected by a person ordinary skilled in the art, and the total amount is preferably 20 to 80% by mass, more preferably 30 to 70% by mass, and even more preferably 35 to 60% by mass, relative to the mass of the cleaning agent composition. Among them, the content of the water-soluble inorganic compound builder is preferably 10 to 50% by mass, more preferably 15 to 45% by mass, and even more preferably 20 to 40% by mass, relative to the mass of the cleaning agent composition. Among them, the content of the water-insoluble inorganic compound builder is preferably 5 to 50% by mass, more preferably 10 to 45% by mass, and even more preferably 15 to 40% by mass, relative to the mass of the cleaning agent composition. Among them, the content of the organic compound builder is preferably 0.1 to 20% by mass, more preferably 0.3 to 15% by mass, and even more preferably 0.5 to 10% by mass, relative to the mass of the cleaning agent composition.

Specific preferred compositions of the cleaning agent composition according to the present invention include the following compositions A to E.

Composition A: 20% by weight of sodium linear alkyl ( $C_{12}$ - $C_{14}$ ) benzenesulfonate, 4% by weight of a nonionic surfactant (polyoxyethylene alkyl ether having 12 to 16 carbon atoms and an average number of added moles of ethylene oxide of 6.0), 30% by weight of sodium carbonate, 10% by weight of sodium sulfate, 30% by weight of zeolite (4A-type zeolite (manufactured by Tosoh Corp.)), 2% by weight of an acrylate-maleate copolymer, and 4% by weight of crystalline silicate (powder SKS-6 (manufactured by Hoechst Tokuyama, Ltd.)).

Composition B: 24% by weight of sodium linear alkyl ( $C_{12}$ - $C_{14}$ ) benzenesulfonate, 5% of linear alkyl ( $C_{10}$ - $C_{13}$ ) sulfuric acid ester sodium, 6% of a fatty acid ( $C_{14}$ - $C_{18}$ ) sodium salt, 7% by weight of a nonionic surfactant (polyoxyethylene alkyl ether having 12 to 16 carbon atoms and an average number of added moles of ethylene oxide of 6.0), 12% of sodium tripolyphosphate, 12% by weight of sodium carbonate, 6% by weight of sodium sulfate, 14% by weight of zeolite (4A-type zeolite (manufactured by Tosoh Corp.)), 6% by weight of sodium polyacrylate (average molecular weight 10,000), and 8% by weight of crystalline silicate (powder SKS-6 (manufactured by Hoechst Tokuyama, Ltd.)).

Composition C: 12% by weight of sodium linear alkyl ( $C_{12}$ - $C_{14}$ ) benzenesulfonate, 11% by weight of a nonionic surfactant (polyoxyethylene alkyl ether having 12 to 16 carbon atoms and an average number of added moles of ethylene oxide of 6.0), 28% by weight of sodium carbonate, 11% by weight of sodium sulfate, 28% by weight of zeolite (4A-type zeolite (manufactured by Tosoh Corp.)), 8% by weight of

sodium polyacrylate (average molecular weight 10,000), and 2% by weight of crystalline silicate (powder SKS-6 (manufactured by Hoechst Tokuyama, Ltd.)).

Composition D: 14% by weight of sodium linear alkyl ( $C_{12}$ - $C_{14}$ ) benzenesulfonate, 2% of a fatty acid ( $C_{14}$ - $C_{18}$ ) sodium salt, 10% by weight of a nonionic surfactant (polyoxyethylene alkyl ether having 12 to 16 carbon atoms and an average number of added moles of ethylene oxide of 6.0), 23% of sodium tripolyphosphate, 29% by weight of sodium carbonate, 6% by weight of sodium sulfate, 11% by weight of zeolite (4A-type zeolite (manufactured by Tosoh Corp.)), 3% by weight of sodium polyacrylate (average molecular weight 10,000), and 2% by weight of crystalline silicate (powder SKS-6 (manufactured by Hoechst Tokuyama, Ltd.)).

Composition E: 20% by weight of a nonionic surfactant (polyoxyethylene alkyl ether having 12 to 16 carbon atoms and an average number of added moles of ethylene oxide of 12.0), 1% by weight of alkylbenzyltrimethylammonium chloride (alkyl group having 8 to 18 carbon atoms), 20% by weight of Softanol 7014 (manufactured by Nippon Shokubai Co., Ltd.), 1.5% by weight of an acrylate-maleate copolymer, 1.5% by weight of monoethanolamine, 1.15% by weight of citric acid, 5% by weight of butyl diglycol, 2% by weight of ethanol, 0.2% by weight of sodium sulfite, and 47.65% by weight of water.

The cleaning agent composition according to the present invention may further include other components such as water, a pH adjusting agent, a buffering agent, a dispersant, an antiseptic, an oxidation inhibitor, an excipient, a dye such as a fluorescent dye, a deodorizer, a deodorant, a fragrance, a softening agent, and a plant extract. The cleaning agent composition according to the present invention may be in any form such as a powder, granules, a compression molded tablet, or a liquid. The cleaning agent composition according to the present invention is such that an amount for one-time use may be packaged in sachets, from the viewpoints of portability or convenience, and in that case, the packaging material is preferably water-soluble.

Although there are no limitations, the cleaning agent composition according to the present invention is preferably intended to be used for garments or for clothing products (sheets, curtains, carpets, wall clothes, and the like). Since the cleaning agent composition according to the present invention contains a mutant alkaline cellulase showing high anti-redeposition ability, the cleaning agent composition can exhibit a satisfactory anti-redeposition effect.

The amount of incorporation of the mutant alkaline cellulase of the present invention into a cleaning agent composition is not particularly limited as long as it is an amount by which the alkaline cellulase exhibits activity. However, the amount of incorporation is preferably 0.1 to 5000 U, more preferably 1 to 3000 U, and even more preferably 10 to 2000 U, per kilogram of the cleaning agent composition.

## EXAMPLES

Hereinafter, the present invention is more specifically described by way of Examples. However, the scope of the present invention is not intended to be limited to these Examples.

Meanwhile, the experimental procedure, reagents and the like that were commonly employed are described first in the following descriptions.

### 1) Amplification of DNA Fragment

The amplification of a DNA fragment was carried out by a polymerase chain reaction (PCR) using a GeneAmp PCR system (Applied Biosystems, Inc.) and using a Pyrobest DNA polymerase (Takara Bio, Inc.) and accessory reagents. The

## 31

reaction liquid composition for PCR was obtained by mixing 1  $\mu$ L of an appropriately diluted template DNA, 20 pmol each of a sense primer and an antisense primer, and 2.5 U of a Pyrobest DNA polymerase, and adding water to the mixture to adjust the total amount of the reaction liquid to 50  $\mu$ L. The PCR reaction was carried out under the conditions of repeating 30 cycles of a three-stage temperature change cycle of 10 seconds at 98° C., 30 seconds at 55° C., and 1 to 5 minutes at 72° C. (the time was adjusted in accordance with the target amplification product, but was adjusted on the basis of 1 minute per kb), and then performing the reaction for 5 minutes at 72° C.

The primers used in the DNA fragment amplifications that will be described below are presented in Table 1-1 to Table 1-3.

TABLE 1-1

Primer name	Primer sequence (5'→3')	SEQ ID NO:
237UB1	TTGCGGATCCAACAGGCTTATATTAGAGGAAATTC	13
S237RV	TCGTACTCCTTTTATTATCG	14
Q71E-RV	ATTTTTTCTCCATGTTCTACTAATGTC	15
Q71E-FW	GACATTAGTAGATGAACATGGAGAAAAAAT	16
S193R-RV	TCCACCATTATTATTACGACTCGGCTCA	17
S193R-FW	TGAGCCGAGTCGTAATAATAATGGTGGA	18
Q242S-RV	AGTCCGGACGCGAATCCAGTTTG	19
Q242S-FW	CAAACGGAGTTCGCGTCCGGAAT	20

TABLE 1-2

Primer name	Primer sequence (5'→3')	SEQ ID NO:
N419A-RV	TTTGGAATCCGAAGCCACTCCAAATCCT	21
N419A-FW	AGGATTGGAGTGGCTTCGATTCTCCAAA	22
D421A-RV	CTTTATTGGAGAAGCCGAATCACTCCA	23
D421A-FW	TGGAGTGAATTCGGCTTCTCCAAATAAAG	24
W454Y-RV	AGACGAGCATTAGCATAGAAGTTGCCATCT	25
W454Y-FW	AGATGGCAACTTCTATGCTAATGCTCGTCT	26
W501Y-RV	CTCTGGATTGCATATCCACTTTTAC	27
W501Y-FW	GTAAAAGTGGATATGCAATCCAGAG	28

TABLE 1-3

Primer name	Primer sequence (5'→3')	SEQ ID NO:
Q58R-RV	ATCGACTTCTTGTAATTCTAATGCGCCA	29
Q58R-FW	TGGCGCATTAGAATTACAAGAAGTCGAT	30
Q58E-RV	ATCGACTTCTTGTAACGTAATGCGCCA	31
Q58E-FW	TGGCGCATTACGTTTACAAGAAGTCGAT	32

## 32

Furthermore, the primer sets for upstream region amplification and for downstream region amplification, which were used to introduce intended amino acid mutations to S237 cellulase or a mutant S237 cellulase in Examples 3 to 5, are presented in Table 2-1 to Table 2-3 (see the Examples described below for the details).

TABLE 2-1

Amino acid mutation to be introduced	Glutamine at position 71 → glutamic acid	Serine at position 193 → arginine
Primer set for upstream region amplification	237UB1 Q71E-RV	237UB1 S193R-RV
Primer set for downstream region amplification	Q71E-FW S237RV	S193R-FW S237RV

TABLE 2-2

Amino acid mutation to be introduced	Asparagine at position 419 → alanine	Aspartic acid at position 421 → alanine	Tryptophan at position 454 → tyrosine	Tryptophan at position 501 → tyrosine
Primer set for upstream region amplification	237UB1 N419A-RV	237UB1 D421A-RV	237UB1 W454Y-RV	237UB1 W501Y-RV
Primer set for downstream region amplification	N419A-FW S237RV	D421A-FW S237RV	W454Y-FW S237RV	W501Y-FW S237RV

TABLE 2-3

Amino acid mutation to be introduced	Glutamine at position 58 → arginine	Glutamine at position 58 → glutamic acid	Glutamine at position 242 → serine
Primer set for upstream region amplification	237UB1 Q58R-RV	237UB1 Q58E-RV	237UB1 Q242S-RV
Primer set for downstream region amplification	Q58R-FW S237RV	Q58E-FW S237RV	Q242S-FW S237RV

2) Gene Introduction into *Bacillus subtilis*

The introduction of a gene encoding S237 cellulase or a mutant S237 cellulase into *Bacillus subtilis* was carried out according to any one of a competent cell transformation method (J. Bacteriol. 93, 1925 (1967)), an electroporation method (FEMS Microbiol. Lett. 55, 135 (1990)), and a protoplast transformation method (Mol. Gen. Genet. 168, 111 (1979)).

In the competent cell transformation method, first, *Bacillus subtilis* (*Bacillus subtilis* Marburg No. 168 (Nature, 390, (1997), p. 249)) was cultured by shaking in SPI medium (0.20% ammonium sulfate, 1.40% dipotassium hydrogen phosphate, 0.60% potassium dihydrogen phosphate, 0.10% trisodium citrate dihydrate, 0.50% glucose, 0.02% casamino acid (Difco Laboratories, Inc.), 5 mM magnesium sulfate, 0.25 manganese chloride, and 50  $\mu$ g/ml tryptophan) at 37° C., until the degree of growth (OD600) reached about 1. After the shaking, a portion of the culture fluid was inoculated into a 9-fold amount of SPII medium (0.20% ammonium sulfate, 1.40% dipotassium hydrogen phosphate, 0.60% potassium dihydrogen phosphate, 0.10% trisodium citrate dihydrate, 0.50% glucose, 0.01% casamino acid (Difco Laboratories, Inc.), 5 mM magnesium sulfate, 0.40  $\mu$ M manganese chloride, and 5  $\mu$ g/ml tryptophan), and the cells were further

cultured by shaking until the degree of growth (OD600) reached about 0.4. Thus, *Bacillus subtilis* cells were prepared as competent cells. Subsequently, in 100  $\mu$ L of the competent cell suspension thus prepared (competent cell culture in SPII medium), 2  $\mu$ L of a solution containing a plasmid vector having a gene encoding S237 cellulase or a gene encoding a mutant S237 cellulase was added, and the mixture was shaken for additional one hour at 37° C. Subsequently, the entire amount was spreaded on LB agar medium (1% tryptone, 0.5% yeast extract, 1% NaCl, and 1.5% agar) containing suitable antibiotics for selection. The cells were statically cultured at 37° C., and then grown colonies were isolated as a transformant.

In the protoplast transformation method, first, a *Bacillus subtilis* strain (*Bacillus subtilis* Marburg No. 168 (Nature, 390, (1997), p. 249)) was cultured by shaking in 50 mL of LB medium (1% tryptone, 0.5% yeast extract, and 1% NaCl) at 37° C. for about 2 hours, and at the time point at which the absorbance at 600 nm reached 0.4, the bacterial cells were collected by centrifugation (7000 rpm, for 15 minutes) at room temperature. The collected bacterial cells were suspended in 5 mL of SMMP [0.5 M sucrose, 20 mM disodium maleate, 20 mM magnesium chloride hexahydrate, and 35% (w/v) Antibiotic Medium 3 (Difco Laboratories, Inc.)], and then 500  $\mu$ L of a lysozyme solution (30 mg/mL) dissolved in SMMP solution was added to the suspension. The mixture was incubated at 37° C. for one hour to convert the bacterial cells to protoplasts. After completion of the incubation, the protoplasts were collected by centrifugation (2800 rpm, for 15 minutes) at room temperature and were suspended in 5 mL of SMMP to prepare a protoplast solution. To 0.5 mL of the protoplast solution, 10  $\mu$ L of a plasmid solution (containing a plasmid vector which included a gene encoding S237 cellulase or a gene encoding a S237 cellulase variant) and 1.5 mL of 40% (w/v) polyethylene glycol (PEG8000, Sigma-Aldrich Co.) were added, and the mixture was gently stirred and left to stand for 2 minutes at room temperature. Immediately, 5 mL of a SMMP solution was mixed into the mixture, and the protoplasts were collected by centrifugation (2800 rpm, for 15 minutes) at room temperature and were resuspended in 1 mL of a SMMP solution. The protoplast suspension was shaken (120 rpm) for 90 minutes at 37° C., and then the suspension was applied on DM3 regeneration agar medium [0.8% (w/v) agar (Wako Pure Chemical Industries, Ltd.), 0.5% disodium succinate hexahydrate, 0.5% casamino acid technical (Difco Laboratories, Inc.), 0.5% yeast extract, 0.35% monopotassium phosphate, 0.15% dipotassium phosphate, 0.5% glucose, 0.4% magnesium chloride hexahydrate, 0.01% bovine serum albumin (Sigma-Aldrich Co.), 0.5% carboxymethyl cellulose, 0.005% trypan blue (Merck GmbH), and an amino acid mixture liquid (10  $\mu$ g/mL each of tryptophan, leucine and methionine)] containing tetracycline (15  $\mu$ g/mL, Sigma). The protoplasts were cultured for 72 hours at 30° C., and grown colonies were isolated as a transformant.

In the culture of the transformants for production of recombinant protein in the Examples described below, LB medium (1% tryptone, 0.5% yeast extract, and 1% NaCl) was used as a medium for seed culture, and 2 $\times$ YT medium (1.6% tryptone, 1% yeast extract, and 0.5% NaCl) or 2 $\times$ L-maltose medium (2% tryptone, 1% yeast extract, 1% NaCl, 7.5% maltose, and 7.5 ppm manganese sulfate tetra- or pentahydrate) was used as a medium for main culture.

### 3) Preparation of Cleaning Agent Composition

In the evaluation of the anti-redeposition ability, a cleaning agent of the preferred composition C or E described above, or IEC-A detergent (composition F) supplied from Wfk

Testgewebe GmbH (D-41379, Germany) was used as the cleaning agent composition. In the evaluation of an enzyme stability test, a cleaning agent of the composition E was used.

### 4) Evaluation of Anti-Redeposition Ability

The evaluation of the anti-redeposition ability was carried out according to the detergency evaluation method described in JIS K3362: 1998, as follows. 0.33 g of a cleaning agent composition was dissolved in 50 mL of water (in the case of 4° DH, CaCl<sub>2</sub>: 55.42 mg/L, MgCl<sub>2</sub>·6H<sub>2</sub>O: 43.51 mg/L; in the case of 12° DH, CaCl<sub>2</sub>: 166.26 mg/L, MgCl<sub>2</sub>·6H<sub>2</sub>O: 130.53 mg/L), and 0.125 g of carbon black (Asahi Carbon Black for cleaning, manufactured by Asahi Carbon Co., Ltd., or Carbon Black #4000B, MA100 or #40, manufactured by Mitsubishi Chemical Corp.) as a model for hydrophobic soot stain was added to the solution. 50 mL of water (CaCl<sub>2</sub>: 55.42 mg/L, MgCl<sub>2</sub>·6H<sub>2</sub>O: 43.51 mg/L) was added to the mixture, and then the mixture was exposed with ultrasonic waves at 26 $\pm$ 1.5 kHz for 5 minutes to uniformly disperse the components. 400 mL of water (CaCl<sub>2</sub>: 55.42 mg/L, MgCl<sub>2</sub>·6H<sub>2</sub>O: 43.51 mg/L) at 20° C. was further added to the dispersion liquid, and a predetermined amount of alkaline cellulase (S237 cellulase or mutant S237 cellulase) was added to the mixture. This was used as washing water. The washing water thus prepared was transferred into the sample cup of an agitation-type detergency tester, Terg-O-To meter; Ueshima Seisakusho Co., Ltd.) at 20° C. As a cloth for evaluation, 5 sheets of a white cotton cloth (#2003 white woven fabric, 100% cotton, supplied by Tanigashira Shoten (4-11-15, Komatsu, Higashiyo-dogawa-ku, Osaka-shi, Osaka-fu, Japan)) having a size of 6 cm $\times$ 6 cm were placed in the sample cup. In order to further adjust the amount of cloth (bath ratio) relative to the solution, an appropriate amount of a white knitted cotton cloth [seared bleached cloth (supplied by Tanigashira Shoten) that had been washed and then sufficiently rinsed] was introduced to the sample cup, and the contents were stirred for 10 minutes at a rotation speed of 80 $\pm$ 4 rpm. Subsequently, the white cotton cloth was removed together with the white knitted cotton cloth, and the clothes were lightly wrung out and then rapidly introduced into 2000 mL of tap water. Only the white cotton cloth was taken out therefrom, and then the cloth was rinsed for 3 minutes under flowing tap water and was subjected to dehydration and finish ironing. The reflection ratio at 550 nm of the white cotton cloth was measured using a spectrophotometer, CM-3500d (Konica Minolta Holdings, Inc.) (the samples are referred to as enzyme-added group). For the white cotton cloth, the reflection ratio at 550 nm was measured in advance before the washing test, using a spectrophotometer, CM-3500d (Konica Minolta Holdings, Inc.). A control experiment was carried out by the same procedure, except that no alkaline cellulase was added to the dispersion liquid (non-enzyme-added group).

The anti-redeposition ratio for each of the washing test was calculated by the following formula, based on the reflection ratio thus obtained.

$$\text{Anti-redeposition ratio (\%)} = \left\{ \frac{\text{Reflection ratio of white cotton cloth after test}}{\text{Reflection ratio of white cotton cloth before test}} \right\} \times 100 \quad [\text{Mathematical formula 5}]$$

Subsequently, the effect of enzyme addition on the preventing of redeposition, that is, the degree of promotion of anti-redeposition as a result of the addition of an alkaline cellulase enzyme, was calculated by the following formula, based on the anti-redeposition ratio thus calculated. In the Examples described below, the anti-redeposition ability of the added alkaline cellulase was evaluated by using this degree of promotion of anti-redeposition (%) as an index.

35

Degree of promotion of anti-redeposition by enzyme addition (%) =  $\frac{\{(\text{Anti-redeposition ratio of enzyme-added group}) - (\text{anti-redeposition ratio of non-enzyme-added group})\}}{\{100 - (\text{anti-redeposition ratio of non-enzyme-added group})\}} \times 100$  [Mathematical formula 6]

Furthermore, the effect of mutagenesis in the alkaline cellulase on the anti-redeposition ability of the enzyme, that is, the degree of anti-redeposition ability enhancement in the mutant alkaline cellulase, was calculated by the following formula. Meanwhile, the mutant enzyme was a mutant alkaline cellulase into which an intended amino acid substitution had been introduced, and the control enzyme was a parent alkaline cellulase, that is, a wild-type alkaline cellulase or an alkaline cellulase before substitution of the amino acid residue.

Degree of anti-redeposition ability enhancement (%) for mutant alkaline cellulase =  $\frac{\{(\text{Anti-redeposition ratio of mutant enzyme-added group}) - (\text{anti-redeposition ratio of control enzyme-added group})\}}{\{100 - (\text{anti-redeposition ratio of control enzyme-added group})\}} \times 100$  [Mathematical formula 7]

### 5) Evaluation of Anti-Redeposition Ability of *Bacillus* sp. Strain KSM-S237-Derived Alkaline Cellulase (S237 Cellulase)

#### (1. Recombinant Production of S237 Cellulase)

A nucleic acid fragment (3.1 kb) including an alkaline cellulase gene that encodes S237 cellulase (SEQ ID NO: 2) derived from *Bacillus* sp. strain KSM-S237 (FERM BP-7875) [hereinafter, also referred to as S237 cellulase gene; the base sequence is available based on GenBank Accession No. AB18420 (SEQ ID NO: 1); Hakamada et al., Biosci. Biotechnol. Biochem., 64(11), (2000) p. 2281-2289; JP-A No. 2000-210081] was amplified according to the procedure of the section "1) Amplification of DNA fragment" as described above, using a primer set consisting of primers 237UB1 and S237RV indicated in the above Table 1-1. As a template DNA, the genomic DNA extracted from the strain KSM-S237 by a routine method was used.

The amplified fragment was inserted into the *Sma*I restriction enzyme cleavage site of a shuttle vector, pHY300PLK (Yakult Honsha Co., Ltd.; Ishiwa, H. & Shibahara, H., Jpn. J. Genet. (1985) 60, p. 235-243), and thus a recombinant plasmid, pHY-S237, was constructed. The sequence of the S237 cellulase gene fragment inserted into the plasmid was determined by using a 3100 DNA Sequencer (Applied Biosystems, Inc.), and thereby, confirmed that the fragment had the base sequence set forth in SEQ ID NO: 1. Subsequently, *Bacillus subtilis* (*Bacillus subtilis* Marburg No. 168 (Nature, 390, (1997) p. 249)) was transformed using the recombinant plasmid, pHY-S237, according to the section "2) Gene introduction into *Bacillus subtilis*" by protoplast transformation method. The transformant thus obtained was cultured overnight by shaking at 30° C. in 10 mL of LB medium (1% tryptone, 0.5% yeast extract, and 1% NaCl), and 0.05 mL of this culture fluid was inoculated into 50 mL of 2xL-maltose medium (2% tryptone, 1% yeast extract, 1% NaCl, 7.5% maltose, 7.5 ppm manganese sulfate tetra- or pentahydrate, and 15 ppm tetracycline) and was cultured by shaking for 3 days at 30° C. A supernatant of the culture fluid, from which bacterial cells had been removed by centrifugation, was diluted 10 times with deionized water, and then the diluted solution was loaded in a DEAE-Toyopearl 650C (Tosoh Corp.) column (1 cmx3 cm) which had been equilibrated with a 20 mM sodium phosphate buffer solution (pH 6.0). The column was washed with 10 mL of a 20 mM sodium phosphate buffer solution (pH 6.0) containing 0.075 M NaCl, and then proteins were eluted from the column using 10 mL of a

36

20 mM sodium phosphate buffer solution (pH 6.0) containing 0.4 M NaCl. The target recombinant S237 cellulase was eluted as an electrophoretically almost single component. The eluted sample was dialyzed against a 10 mM Tris hydrochloride buffer solution (pH 7.5) containing 1 mM CaCl<sub>2</sub>, and was subjected to desalting treatment. Subsequently, the content of the alkaline cellulase was measured by the following method. That is, 50 μL of 0.4 mM p-nitrophenyl-β-D-cellobioside (Seikagaku Corp.) was added and mixed into 50 μL of the sample solution which had been appropriately diluted with a 1/7.5 M phosphate buffer solution (pH 7.4, Wako Pure Chemical Industries, Ltd.), and the amount of p-nitrophenol released when the reaction had been carried out at 30° C. was quantified based on the change of absorbance at 420 nm (OD420). The amount of the enzyme that releases 1 μmol of p-nitrophenol for one minute was defined as 1 U. Further, the amount of proteins was measured by using a Protein Assay Rapid Kit (manufactured by Wako Pure Chemical Industries, Ltd.) and the bovine serum albumin included in the kit as a standard, using.

A sample containing the recombinant S237 cellulase thus obtained (wild-type S237 cellulase) was subjected to evaluation of the anti-redeposition ability as described below. The evaluation was carried out by adding an enzyme protein in an amount equivalent to 26.4 mU, 52.8 mU, 106 mU, 211 mU or 264 mU, to 500 mL of the washing system.

#### (2. Anti-Redeposition Ability Evaluation Using Various Carbon Blacks)

The anti-redeposition ability of S237 cellulase was evaluated by using various carbon blacks. As the carbon blacks, 4 kinds of carbon blacks such as Asahi carbon black for cleaning manufactured by Asahi Carbon Co., Ltd., and Carbon Black #4000B, MA100 and #40 manufactured by Mitsubishi Chemical Corp. were used.

Prior to the anti-redeposition ability evaluation, the characteristics of each of the carbon blacks (hydrophobicity, and the acidic functional group content) were investigated as follows. 100 mL of an aqueous solution of 0.1% (w/v) polyoxyethylene (average number of added moles of EO 6) alkyl (C<sub>12</sub>-C<sub>14</sub>) ether was charged into a 100-mL beaker (Iwaki Co., Ltd.), 0.1 g of each carbon black powder was dropped from 10 cm above the surface of the aqueous solution to the surface, and the time necessary for settling the entire amount of the powder was measured. Measurement was repeated three times, and as a result, the time for settling was 4.9±0.6 seconds for #4000B, 14.1±1.0 seconds for MA100, and 60.5±4.6 seconds for #40. For a portion of the Asahi carbon black for cleaning was staying on the surface of the aqueous solution even after a lapse of 10 minutes or longer, and the time necessary for the entire amount to be wetted was 78.8±9.1 seconds. According to these results, it was found that among the various carbon blacks, hydrophobicity of #4000B was the lowest, followed by MA100 and #40 in this order, and hydrophobicity of the Asahi carbon black for cleaning was the highest. Subsequently, each of carbon black suspensions was exposed to ultrasonication at 26±1.5 kHz for 5 minutes, and while the suspension was thoroughly stirred, pH was measured. The pH of an aqueous solution of 0.1% (w/v) polyoxyethylene (average number of added moles of EO 6) alkyl (C<sub>12</sub>-C<sub>14</sub>) ether containing no carbon black was 4.75, and was 4.97 for #4000B, 4.69 for MA100, 4.81 for #40, and 4.86 for Asahi carbon black for cleaning after each of the carbon black was dispersed therein. pH of the dispersion liquid was decreased as a result of addition of MA100, the result suggests that MA100 contains the largest number of acidic functional groups (it may be considered that a majority of the functional groups are carboxyl groups), of the other

hand, #4000B contains the smallest acidic functional group content among the carbon blacks investigated.

Considering the characteristics of various carbon blacks as described above, an evaluation of the anti-redeposition ability was carried out according to the section "4) Evaluation of anti-redeposition ability" described above. The results obtained by using a cleaning agent having the composition C and adding S237 cellulase in an enzyme amount equivalent to 0 mU, 106 mU or 264 mU, are shown in Table 3 (anti-redeposition ratio) and Table 4 (degree of promotion of anti-redeposition).

TABLE 3

Enzyme added (mU/500 mL)	Anti-redeposition ratio (%)							
	Asahi cleaning		#40		MA100		#4000B	
	Mean value	Standard deviation	Mean value	Standard deviation	Mean value	Standard deviation	Mean value	Standard deviation
0	62.6	2.8	77.6	1.0	74.0	1.0	83.4	0.5
106	76.1	1.1	81.3	0.9	78.8	1.0	85.4	0.7
264	78.2	0.5	81.9	1.3	80.4	0.9	85.6	0.6

TABLE 4

Enzyme added (mU/500 mL)	Degree of promotion of anti-redeposition due to enzyme addition (%)			
	Asahi cleaning	#40	MA100	#4000B
106	36.2	16.8	18.6	11.7
264	41.6	19.1	24.8	13.3

As shown in Table 4, an effect of promoting prevention of the redeposition caused by any of the carbon blacks, as a result of the addition of S237 cellulase, was observed. The most significant anti-redeposition promoting effect was exhibited by Asahi carbon black for cleaning, and followed by MA100, #40 and #4000B in this order, with slight differences. These results of order suggest that the effect of promoting the preventing of redeposition due to the addition of S237 cellulase is greatly affected by degree of hydrophobicity of the carbon black.

Furthermore, for a comparison, an evaluation of the anti-redeposition ability was carried out by the same method as described above, except that a protease, an amylase or a lipase as another type of hydrolase, and Endolase (Novozymes, Inc.) and Carezyme (Novozymes, Inc.) as another type of cellulase were used instead of S237 cellulase. Protein amounts of these enzymes were equivalent to concentrations of 26.4 mU, 52.8 mU and 211 mU. As the carbon black, Asahi carbon black for cleaning manufactured by Asahi Carbon Co., Ltd. was used. For a control experiment, an evaluation of the anti-redeposition ability was carried out under the same conditions using S237 cellulase. The results are shown in FIG. 2.

As a result, when a protease, an amylase or a lipase was used, the anti-redeposition ratios of the enzyme-added group and the non-enzyme-added group were all approximately 52%, without a significant difference, and the anti-redeposition promoting effect caused by the addition of these enzymes was not observed. On the other hand, when S237 cellulase was used, an increase in the anti-redeposition ratio was observed along with increase of amount of the enzyme addition, and therefore, the anti-redeposition promoting effect was confirmed.

When each of Endolase (Novozymes, Inc.) and Carezyme (Novozymes, Inc.) was used, the anti-redeposition ratio gradually increased along with increase of amount of the enzyme addition. However, when compared with S237 cellulase, the degree of the increase was small, and the anti-redeposition promoting effect was small. On the other hand, when S237 cellulase was used, anti-redeposition promoting effect, that was twice or more than that of Endolase, which exhibited a higher anti-redeposition promoting effect than Carezyme, was observed. These results suggest that S237

cellulase provides high anti-redeposition promoting effect which is not observed when other enzymes are used.

### (3. Investigation of pH Dependency of Anti-Redeposition Promoting Effect)

The effect of pH of washing water on the anti-redeposition promoting effect caused by enzyme addition was investigated as follows. An evaluation was carried out according to the anti-redeposition ability evaluation method described above, by using a cleaning agent of the composition E, and S237 cellulase in an enzyme amount equivalent to 0 mU or 52.8 mU, with the proviso that the pH of the cleaning liquid was adjusted to 8.0, 4.3, 4.1 or 3.6 by adding sulfuric acid.

As a result, as shown in FIG. 3, the anti-redeposition promoting effect was slightly decreased at pH 4.1, and was largely decreased at pH 3.6. Even in consideration of the fact disclosed in Patent Document 1 (which describes an invention related to S237 cellulase) that the pH stability of S237 cellulase greatly decreases near pH 4 (FIG. 3 in Patent Document 1), the above-described results suggest that the anti-redeposition ability possessed by S237 cellulase is largely impaired under the conditions where an irreversible structural change will occur, such as pH decrease. Furthermore, S237 cellulase would hardly exhibit any activity under the conditions of pH 5 or lower (FIG. 5 in Patent Document 1), however the anti-redeposition promoting effect at pH 4.3 was recognized to be almost equivalent to the effect at pH 8. These findings suggest that the anti-redeposition promoting effect of S237 cellulase originates from the structure of the enzyme.

According to the evaluation of anti-redeposition ability described above, the promoting effect of less hydrophobic MA100 was found to be equal to or higher than the effect of #40, suggesting that the anti-redeposition ability of S237 cellulase is affected by the content of the acidic functional groups of carbon black, that is, the abundance of negative charge factors. Therefore, it could be considered that the anti-redeposition ability of S237 cellulase is dependent on the physical repulsion between S237 cellulase and hydrophobic substances (repulsion between hydrophilic groups and hydrophobic groups+electrostatic repulsion).

Furthermore, it was speculated, based on the results obtained from the investigation of pH dependency as described above, that when the properties derived from the structure of S237 cellulase are modified, the anti-redeposition ability may be enhanced.



Specifically, it was conceived that when the hydrophilicity of the enzyme surface is further increased while the basic structure of S237 cellulase is maintained, high repulsion is caused between the enzyme surface and hydrophobic carbon black, and consequently, the anti-redeposition ability of S237 cellulase can be enhanced (see FIG. 1B).

#### 6) Steric Structure Modeling of S237 Cellulase

In order to increase the hydrophilicity of the enzyme surface of S237 cellulase, a method may be employed wherein a position which has less influence on the overall structure of S237 cellulase, even if the position is substituted, is selected among the positions on the amino acid sequence where non-charged amino acid residues that are exposed to the enzyme surface in S237 cellulase are present, and the non-charged amino acid residue at the position is substituted with a charged amino acid residue. Thus, in order to select suitable positions for substitution, at first, a steric structure model of S237 cellulase was constructed as described below.

Steric structure modeling of the catalytic domain of S237 cellulase was carried out by the following procedure, using steric structures of the catalytic domain of *Bacillus* sp. strain KSM-635-derived alkaline cellulase (635 cellulase) (registered in Protein Data Bank (PDB); 1G01 and 1G0C) as models. IRIS Indigo2 Extreme was used as the computer, and insightII (Ver. 95.5) was used as a graphical user interface program. The structure of S237 cellulase was constructed based on the structure of 635 cellulase, using a module of insightII, modeler 4. That is, the topology of the S237 cellulase sequence was produced by referring to the coordinates of 635 cellulase, and for the atoms for which the coordinates could not be defined, allocation of the coordinates was carried out by referring to a residue topology file (RTF) of a polymer system modeling program, CHARMM (accessible from Chemistry at HARvard Macromolecular Mechanics, <http://www.charmm.org/>). Subsequently, the restraint on the structure of S237 cellulase was calculated as a probability density function (PDF), based on the alignment between the amino acid sequence of 635 cellulase and the amino acid sequence of S237 cellulase. The number of models thus produced was previously fixed at 1, for producing models that satisfy as many restraints as possible. Optimization of the models by a variable target function method (VTF) was carried out as follows. First, only those restraints that can be easily optimized (in which corresponding atoms are closely positioned each other) were selected, and energy minimization was carried out by a conjugate gradient method. Subsequently, these steps were repeated for other restraint conditions also, and finally, energy minimization according to a conjugate gradient method was performed for all restraints. Next, model optimization by simulated annealing was carried out. Energy minimization according to a conjugate gradient method, simulated annealing (heating conditions (Heating)→cooling conditions (Cooling)), and energy minimization according to a conjugate gradient method were carried out by using an optimization protocol "Low" (based on maximum speed molecular dynamic simulated annealing), under the conditions in which only those restraints that did not satisfy the conditions and the atoms corresponding thereto were selected, while other atoms were fixed. Subsequently, all the restraints and atoms were selected and energy minimization according to the conjugate gradient method was carried out. The degree of restraint violation was calculated, and after confirming that the level was not particularly irregular, the final model was constructed.

The model thus constructed was subjected to a visualization analysis using the program Discovery Studio Visualizer Ver. 1.5 (Accelrys Software, Inc.). The residue solvent acces-

sibility of each amino acid residue was calculated by performing an analysis using the Solvent Accessibility program of Discovery Studio Visualizer Ver. 1.5, by setting the grid point for each atom at 240, and the probe radius at 1.40.

An amino acid residue having a value of this residue solvent accessibility of 50 or greater was considered as an amino acid residue having a high degree of surface exposure, and the relevant amino acid was appointed as a primary candidate of amino acid residues that can be selected as the objects of substitution in the present invention. From the primary candidates, first, charged amino acid residues were excluded. Next, the 3 amino acid residues in the N-terminal region and the 36 amino acid residues in the C-terminal region, which had low reliability of modeling, were also excluded. Furthermore, in consideration of that the constructed model was a model lacking the cellulose binding module (CBM domain), in the actual steric structure of S237 cellulase, the amino acid residues following the aspartic acid at position 369 (Asp369), which have a possibility of being covered by the CBM domain and not exposed to the surface, were excluded from the candidates for substitution. Furthermore, in the actual steric structure of S237 cellulase, leucine at position 42 (Leu42) to glycine at position 44 (Gly44), which have a possibility of being covered by the amino-terminal region that had been excluded from the constructed model, were excluded from the candidates for substitution. Further, the two tryptophan residues at position 88 and position 240 (Trp88 and Trp240) in the vicinity of the substrate binding pocket of S237 cellulase also have a possibility of participating in the binding with a substrate, and therefore, the tryptophan residues were excluded from the candidates. The asparagine residues at position 250 and position 330 (Asn250 and Asn330), around which both acidic amino acid residues and basic amino acid residues are present, were also excluded from the candidates for substitution. As a result, 55 non-charged amino acid residues were selected as the amino acid residues to be substituted of the present invention. The result suggests that when these non-charged amino acid residues thus selected are substituted with charged amino acid residues, the surface charge of S237 cellulase would be increased, and the anti-redeposition ability of S237 cellulase would be enhanced.

Furthermore, with regard to other cellulases sharing high identity with S237 cellulase, the result suggests that non-charged amino acid residues that are exposed to the enzyme surface may be present at the positions corresponding to these 55 amino acid residues with high possibility, and therefore the anti-redeposition ability of the cellulases would be enhanced by similarly substituting the amino acid residues at those positions with charged amino acid residues.

In the columns for "S237" in the following Table 5, 54 amino acid residues that can be considered as the target for substitution that have been selected as described above in connection with the catalytic domain of S237 cellulase are shown. Furthermore, Table 5 shows amino acid residues of other alkaline cellulases sharing high amino acid sequence identity with S237 cellulase, *Bacillus* sp. strain DSM12648-derived alkaline cellulase (DSM12648 cellulase; SEQ ID NO: 4), *Bacillus* sp. strain 1139-derived alkaline cellulase (1139 cellulase; SEQ ID NO: 6), *Bacillus* sp. strain KSM-64-derived alkaline cellulase (endo-1,4- $\beta$ -glucanase) (64 cellulase; SEQ ID NO: 8), *Bacillus* sp. strain KSM-635-derived alkaline cellulase (KSM-635 cellulase; SEQ ID NO: 10), and *Bacillus* sp. strain N-4-derived alkaline cellulase (endoglucanase) (N4 cellulase; SEQ ID NO: 12), which are aligned to the 55 amino acid residues of S237 cellulase (that is, present at the positions corresponding to those residues) when an align-

ment of the amino acid sequence of each of the cellulases and the amino acid sequence of S237 cellulase is produced (Table 5). Each of the positions of the amino acid residues is indicated by the number of the amino acid residue in the amino acid sequence of the alkaline cellulase set forth in respective sequence ID number.

TABLE 5

S237			DSM12648			1139			64			KSM635			N4		
Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)
45	Asn	N	16	Asn	N	45	Asn	N	44	Asn	N	226	Thr	T	63	Gly	G
52	Ser	S	23	Ser	S	52	Ser	S	51	Ser	S	233	Ser	S	71	Ser	S
56	Ala	A	27	Ala	A	56	Ala	A	55	Ala	A	237	Ala	A	75	Ala	A
58	Gln	Q	29	Gln	Q	58	Gln	Q	57	Gln	Q	239	Gln	Q	77	Gln	Q
60	Gln	Q	31	Gln	Q	60	Gln	Q	59	Gln	Q	241	Val	V	79	Val	V
64	Gly	G	35	Gly	G	64	Gly	G	63	Gly	G	245	Gly	G	83	Gly	G
66	Met	M	37	Met	M	66	Met	M	65	Met	M	247	Met	L	85	Val	V
71	Gln	Q	42	Gln	Q	71	Gln	Q	70	Gln	Q	252	Glu	E	90	Gln	Q
103	Asn	N	74	Asn	N	103	Asn	N	102	Asn	N	284	Asn	N	122	Asn	N
119	Asn	N	90	Asn	N	119	Asn	N	118	Asn	N	300	Asn	N	138	Asn	N
122	Ala	A	93	Ala	A	122	Ala	A	121	Ala	A	303	Ala	A	141	Arg	R
123	Thr	T	94	Ser	S	123	Ser	S	122	Ser	S	304	Thr	T	142	Tyr	Y
124	Asn	N	95	Asn	N	124	Asn	N	123	Asn	N	305	Asn	N	143	Asn	N
125	Pro	P	96	Pro	P	125	Pro	P	124	Pro	P	306	Pro	P	144	Pro	P
127	Leu	L	98	Leu	L	127	Leu	L	126	Leu	L	—	—	—	146	Leu	L
130	Gln	Q	101	Ser	S	130	Ser	S	129	Ser	S	310	Asp	D	148	Glu	E
140	Ile	I	111	Ile	I	140	Ile	I	139	Ile	I	320	Phe	F	158	Lys	K
161	Pro	P	132	Pro	P	161	Pro	P	160	Pro	P	341	Asp	D	179	Asp	D
164	Ala	A	135	Ala	A	164	Ala	A	163	Ala	A	344	Ser	S	193	Leu	L
175	Ala	A	146	Ala	A	175	Ala	A	174	Ala	A	355	Asp	D	204	Glu	E
176	Leu	L	147	Leu	L	176	Leu	L	175	Leu	L	356	His	H	205	Lys	K
178	Pro	P	149	Pro	P	178	Pro	P	177	Pro	P	361	Pro	P	207	Pro	P
179	Asn	N	150	Asn	N	179	Asn	N	178	Asn	N	362	Lys	K	208	Asn	N
181	Pro	P	152	Pro	P	181	Pro	P	180	Pro	P	364	His	H	210	Pro	P
193	Ser	S	164	Ser	S	193	Ser	S	192	Ser	S	376	Pro	P	222	Ser	S
194	Asn	N	165	Asn	N	194	Asn	N	193	Asn	N	377	Asn	N	223	Asn	N
195	Asn	N	166	Asn	N	195	Asn	N	194	Asn	N	378	Asn	N	224	Ser	S
196	Asn	N	167	Asn	N	196	Asn	N	195	Asn	N	379	Asn	N	225	Ser	S
197	Gly	G	168	Gly	G	197	Gly	G	196	Gly	G	380	Gly	G	226	Gly	G
199	Ala	A	170	Ala	A	199	Ala	A	198	Ala	A	382	Pro	P	228	Pro	P
202	Pro	P	173	Pro	P	202	Pro	P	201	Pro	P	385	Thr	T	231	Thr	T
203	Asn	N	174	Asn	N	203	Asn	N	202	Asn	N	386	Asn	N	232	Asn	N
217	Pro	P	188	Pro	P	217	Pro	P	216	Pro	P	400	Pro	P	246	Pro	P
225	Ser	S	196	Ser	S	225	Ser	S	224	Ser	S	408	Lys	K	254	Ser	S
227	Asn	N	198	Asn	N	227	Asn	N	226	Asn	N	—	—	—	256	Asn	N
228	Ala	A	199	Ala	A	228	Ala	A	227	Ala	A	—	—	—	257	Ala	A
251	Pro	P	222	Pro	P	251	Pro	P	250	Pro	P	431	Pro	P	281	Pro	P
267	Ser	S	238	Ser	S	267	Ser	S	266	Ser	S	447	Ser	S	297	Thr	T
272	Thr	T	243	Thr	T	272	Thr	T	271	Thr	T	452	His	H	302	Asn	N
276	Pro	P	247	Pro	P	276	Pro	P	275	Pro	P	456	Pro	P	306	Pro	P
277	Ser	S	248	Pro	P	277	Pro	P	276	Pro	P	457	Glu	E	307	Glu	E
280	Pro	P	251	Pro	P	280	Pro	P	279	Pro	P	460	Pro	P	310	Ser	S
282	Ser	S	253	Ser	S	282	Ser	S	281	Ser	S	462	Ser	S	312	Glu	E
297	Asn	N	268	Asn	N	297	Asn	N	296	Asn	N	477	Asn	N	327	Lys	K

TABLE 5-continued

S237			DSM12648			1139			64			KSM635			N4		
Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)
310	Gln	Q	281	Gln	Q	310	Gln	Q	309	Gln	Q	490	Gln	Q	340	Glu	E
312	Ser	S	283	Asn	N	312	Asn	N	311	Asn	N	492	Asn	N	342	Asp	D
318	Tyr	Y	289	Tyr	Y	318	Tyr	Y	317	Tyr	Y	498	Tyr	Y	348	Tyr	Y
324	Val	V	295	Val	V	324	Val	V	323	Val	V	504	Val	V	354	Val	V
345	Asn	N	316	Asn	N	345	Asn	N	344	Asn	N	525	Asn	N	375	Asn	N
354	Phe	F	325	Phe	F	354	Phe	F	353	Phe	F	534	Phe	F	384	Phe	F
356	Leu	L	327	Leu	L	356	Leu	L	355	Leu	L	536	Leu	L	386	Leu	L
357	Gly	G	328	Gly	G	357	Gly	G	356	Gly	G	537	Gly	G	387	Asn	N
360	Asn	N	331	Asn	N	360	Asn	N	359	Asn	N	540	Asp	D	390	Asp	D
363	Asn	N	334	Asn	N	363	Ser	S	362	Ser	S	543	Asp	D	393	Asp	D
368	Pro	P	339	Pro	P	368	Pro	P	367	Pro	P	548	Ala	A	398	Glu	E

In Examples 3 and 4 described below, the mutant S237 cellulases in which the amino acid residues at position 71 and position 193 among the non-charged amino acid residues at the positions selected as described above were substituted with charged amino acid residues, were constructed.

7) Investigation of Relationship Between Adsorption Power of Alkaline Cellulase to Cellulose and Anti-Redeposition Ability, and Determination of Amino Acid Residues to be Substituted that Enhance Anti-Redeposition Ability

Promotion of adsorption of the alkaline cellulases to cellulose by addition of sodium chloride was shown according to a method similar to the method of "4) Evaluation of anti-redeposition ability", as follows.

*Bacillus* sp. strain KSM-635-derived alkaline cellulase (635 cellulase) was produced according to methods reported (in Agric. Bio. Chem., 55, 2387, 1991). Subsequently, 0.33 g of a cleaning agent composition was dissolved in 500 mL of water (CaCl<sub>2</sub>: 55.42 mg/L, MgCl<sub>2</sub>·6H<sub>2</sub>O: 43.51 mg/L), and 2110 mU of 635 cellulase, and sodium chloride in an amount of 5% relative to the total amount of the washing water were added to the solution, to obtain a washing water. The washing water thus prepared was transferred into the sample cup of an agitation type detergency tester, Terg-O-To meter; Ueshima Seisakusho Co., Ltd.) at 20° C. As a cloth for evaluation, 5 sheets of a white cotton cloth (#2003 white woven fabric, 100% cotton, supplied by Tanigashira Shoten) having a size of 6 cm×6 cm were placed in the sample cup, and 40 g of a white knitted cotton cloth (seared bleached cloth (supplied by Tanigashira Shoten) that had been washed and then sufficiently rinsed) was introduced to the sample cup. The contents were stirred for 10 minutes at rotation speed of 80±4 rpm. Subsequently, the white cotton cloth was removed together with the white knitted cotton cloth, and the clothes were lightly wrung out and then rapidly introduced into 2000 mL of tap water. Only the white cotton cloth was taken out therefrom, and the cloth was dehydrated without rinsing and then was introduced into a Coomassie Brilliant Blue G staining solution (prepared by dissolving 2.5 g of Coomassie Brilliant Blue G250 (Merck GmbH), 4 g of methanol, and 90 mL of acetic acid in 910 mL of deionized water). After immersion for 30 minutes, the cloth was lightly wrung out and then was transferred into a decolorization solution (prepared by mixing 50 mL of deionized water, 50 mL of methanol and 10 mL of acetic acid). Immersion of the cloth in the decolorization solution for 30 minutes was repeated two times. Subsequently, the cloth was washed with water and was subjected to finish ironing. Then, the brightness (L value) was measured using a spectrophotometer, CM-3500d (Konica Minolta Holdings, Inc.). A control experiment was carried out by the same procedure, except that sodium chloride was not added to the washing water.

As a result, while the L value in the case of non-addition of sodium chloride was 92, the L value in the case of adding sodium chloride in an amount of 5% was 71. Since the L value decreases with the adsorption of proteins to the cloth, this decrease in the L value means an increase in the amount of adsorption of 635 cellulase to the white cotton cloth. That is, it was shown that the adsorption of the alkaline cellulase to cellulose was promoted by the addition of sodium chloride.

Subsequently, the anti-redeposition ability of 635 cellulase in the presence of sodium chloride was evaluated according to the section "4) Evaluation of anti-redeposition ability", using

washing water to which sodium chloride had been added in an amount of 5%. A cleaning agent of the composition B, and 1000 mU of 635 cellulase were used. As the carbon black, Asahi carbon black for cleaning was used. As control experiments, the same evaluation with the proviso that sodium chloride was not added to the washing water, and that no cellulase was added, was carried out.

As a result, the anti-redeposition ratio in the case of adding sodium chloride was 47% in the washing water without any added cellulase, and was 30% in the washing water with an added cellulase, in which a decrease of the anti-redeposition ratio in the presence of a cellulase was observed. On the other hand, in the case where sodium chloride was not added, the anti-redeposition ratio was 72% in the washing water without addition of cellulase, and was 82% in the washing water with addition of cellulase, thus, an increase of the anti-redeposition ratio, in the presence of a cellulase, was observed. Taking into consideration of the above experimental results altogether, the result suggests that since the adsorption of the alkaline cellulase to cellulose was promoted in the presence of sodium chloride, a redeposition promoting effect was rather exhibited.

An alkaline cellulase adsorbs to cellulose via the cellulose binding module (CBM) in the interior of the enzyme. Thus, the result suggests that when the cellulose binding property of the alkaline cellulase via the cellulose binding module is decreased, it would be more difficult for the alkaline cellulase to adsorb to cellulose, therefore, higher anti-redeposition effect would be provided even under the condition where, for example, the cellulose adsorption is promoted (see FIG. 1B).

The cellulose binding module (CBM) of 635 cellulase or S237 cellulase consists of two kinds of CBMs that belong to CBM17 family and CBM28 family. Amino acid residues that directly participate in the binding to cellulose, which are included in the members of those CBM17 and CBM28 families, have already been reported (published as Biochem. J., 361, 35, 2002). For example, for the CBM17 of S237 cellulase, asparagine at position 419, aspartic acid at position 421, tryptophan at position 454, arginine at position 458, glutamine at position 495, tryptophan at position 501, asparagine at position 503, and asparagine at position 551 in the amino acid sequence set forth in SEQ ID NO: 2; and for the CBM28, alanine at position 605, glutamic acid at position 607, alanine at position 641, arginine at position 645, glutamine at position 684, tryptophan at position 691, glutamine at position 693, and isoleucine at position 740 participate in cellulose binding. Therefore, it suggests that when these amino acid residues are substituted with other amino acid residues, the binding property of the alkaline cellulase to cellulose may be weakened. Furthermore, it may be considered that amino acid residues adjacent to these amino acid residues (particularly, two amino acid residues adjacent to the relevant amino acid residues) also participate in cellulose binding either directly or indirectly. Therefore, the result suggests that the cellulose binding property may be weakened by substituting or deleting the amino acid residues that are adjacent to the amino acid residues that directly participate in cellulose binding, or by inserting amino acid residues at the positions more adjacent to the relevant residues. Based on such investigation results, 44 amino acid residues that can be considered as target of substitution so as to weaken the cellulose binding property of the alkaline cellulase are summarized in Table 6.

TABLE 6

S237			DSM12648			1139			64			KSM635			N4		
Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)
418	Val	V	389	Val	V	418	Val	V	417	Val	V	598	Val	V	451	Gln	Q
419	Asn	N	390	Asn	N	419	Asn	N	418	Asn	N	599	Asn	N	452	Asn	N
420	Ser	S	391	Ser	S	420	Gly	G	419	Gly	G	600	Gly	G	453	Ser	S
421	Asp	D	392	Asp	D	421	Asp	D	420	Asp	D	601	Asp	D	454	Asp	D
422	Ser	S	393	Ser	S	422	Ser	S	421	Ser	S	602	Ser	S	455	Ser	S
453	Phe	F	424	Phe	F	452	Tyr	Y	451	Tyr	Y	633	Tyr	Y	486	Tyr	Y
454	Trp	W	425	Trp	W	453	Trp	W	452	Trp	W	634	Trp	W	487	Trp	W
455	Ala	A	426	Ala	A	454	Ala	A	453	Ala	A	635	Asp	D	488	Ser	S
457	Ala	A	428	Ala	A	456	Ala	A	455	Ala	A	637	Val	V	490	Val	V
458	Arg	R	429	Arg	R	457	Arg	R	456	Arg	R	638	Arg	R	491	Arg	R
459	Leu	L	430	Leu	L	458	Leu	L	457	Leu	L	639	Leu	L	492	Ile	I
494	Pro	P	465	Pro	P	493	Pro	P	492	Pro	P	674	Pro	P	527	Pro	P
495	Gln	Q	466	Gln	Q	494	Gln	Q	493	Gln	Q	675	Gln	Q	528	Gln	Q
496	Ser	S	467	Ser	S	495	Gly	G	494	Gly	G	676	Gly	G	529	Ser	S
500	Gly	G	471	Gly	G	499	Asn	N	498	Asn	N	680	Gly	G	533	Glu	E
501	Trp	W	472	Trp	W	500	Trp	W	499	Trp	W	681	Trp	W	534	Trp	W
502	Ala	A	473	Ala	A	501	Val	V	500	Val	V	682	Ala	A	535	Ala	A
503	Asn	N	474	Asn	N	502	Asn	N	501	Asn	N	683	Asn	N	536	Asn	N
504	Pro	P	475	Pro	P	503	Pro	P	502	Pro	P	684	Pro	P	537	Ala	A
550	Asn	N	521	Asn	N	548	Asn	N	547	Asn	N	729	Ser	S	583	Asn	N
551	Asn	N	522	Asn	N	549	Asn	N	548	Asn	N	730	Asn	N	584	Asn	N
552	Ile	I	523	Ile	I	550	Ile	I	549	Ile	I	731	Ile	I	585	Ile	I
604	Trp	W	575	Trp	W	602	Trp	W	601	Trp	W	783	Trp	W	639	Trp	W
605	Ala	A	576	Ala	A	603	Ala	A	602	Ala	A	784	His	H	640	Asp	D
606	Gly	G	577	Gly	G	604	Gly	G	603	Gly	G	785	Thr	T	641	Ser	S
607	Glu	E	578	Glu	E	605	Glu	E	604	Glu	E	786	Glu	E	642	Glu	E
608	Ser	S	579	Ser	S	606	Ser	S	605	Ser	S	787	Ser	S	643	Ser	S
640	Trp	W	611	Trp	W	638	Trp	W	637	Trp	W	819	Trp	W	675	Trp	W
641	Ala	A	612	Ala	A	639	Ala	A	638	Ala	A	820	Ala	A	676	Ala	A
642	Thr	T	613	Thr	T	640	Thr	T	639	Thr	T	821	Thr	T	677	Thr	T
644	Pro	P	615	Pro	P	642	Pro	P	641	Pro	P	823	Pro	P	679	Pro	P
645	Arg	R	616	Arg	R	643	Arg	R	642	Arg	R	824	Arg	R	680	Arg	R
646	Leu	L	617	Leu	L	644	Leu	L	643	Leu	L	825	Leu	L	681	Leu	L
683	Phe	F	654	Phe	F	681	Phe	F	680	Phe	F	862	Phe	F	720	Phe	F
684	Gln	Q	655	Gln	Q	682	Gln	Q	681	Gln	Q	863	Gln	Q	721	Gln	Q
685	Pro	P	656	Pro	P	683	Pro	P	682	Pro	P	864	Pro	P	722	Pro	P
690	Tyr	Y	661	Tyr	Y	688	Tyr	Y	687	Tyr	Y	869	Tyr	Y	727	Tyr	Y

TABLE 6-continued

S237			DSM12648			1139			64			KSM635			N4		
Amino acid position	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid (3-letter code)	Amino acid (1-letter code)	Amino acid (3-letter code)
691	Trp	W	662	Trp	W	689	Trp	W	688	Trp	W	870	Trp	W	728	Trp	W
692	Val	V	663	Val	V	690	Val	V	689	Val	V	871	Gln	Q	729	Ala	A
693	Gln	Q	664	Gln	Q	691	Gln	Q	690	Gln	Q	872	Gln	E	730	Gln	Q
694	Ala	A	665	Ala	A	692	Ala	A	691	Ala	A	873	Val	V	731	Ala	A
739	Met	M	710	Met	M	737	Met	M	736	Met	M	919	Leu	L	775	Leu	L
740	Ile	I	711	Ile	I	738	Ile	I	737	Ile	I	920	Leu	L	776	Ile	I
741	Ile	I	712	Ile	I	739	Ile	I	738	Ile	I	921	Ile	I	777	Phe	F

## 53

In the column for "S237" in Table 6, 44 amino acid residues that may be considered as targets of substitution in the cellulose binding module of S237 cellulase, are shown. Furthermore, Table 6 shows amino acid residues, of other alkaline cellulases sharing high amino acid sequence identity with S237 cellulase, *Bacillus* sp. strain DSM12648-derived alkaline cellulase (DSM12648 cellulase; SEQ ID NO: 4), *Bacillus* sp. strain 1139-derived alkaline cellulase (1139 cellulase; SEQ ID NO: 6), *Bacillus* sp. strain KSM-64-derived alkaline cellulase (endo-1,4- $\beta$ -glucanase) (64 cellulase; SEQ ID NO: 8), *Bacillus* sp. strain KSM-635-derived alkaline cellulase (KSM-635 cellulase; SEQ ID NO: 10), and *Bacillus* sp. strain N-4-derived alkaline cellulase (endoglucanase) (N4 cellulase; SEQ ID NO: 12), which are aligned to the 44 amino acid residues of S237 cellulase (that is, present at the positions corresponding to those residues) when an alignment of the amino acid sequence of each of the cellulases and the amino acid sequence of S237 cellulase is produced. Each of the positions of the amino acid residues is indicated with the number of the amino acid residue in the amino acid sequence of the alkaline cellulase set forth in the corresponding sequence ID number.

In Examples 5 and 6 described below, mutant S237 cellulases in which some amino acid residues among such amino acid residues that participate in cellulose binding (in Table 6, underlined residues, namely, the amino acid residues at the positions 419, 421, 454 and 501) were substituted with other amino acid residues, were constructed.

## Example 1

## Production of Mutant S237 Cellulase-1

A mutant S237 cellulase in which glutamine at position 58 of S237 cellulase (SEQ ID NO: 2) was substituted with arginine (S237-Q58R) was produced by introducing a nucleotide mutation to the S237 cellulase gene and recombinantly expressing the mutant, as follows.

PCR amplification was carried out according to the section "1) Amplification of DNA fragment", using, as a template, the genomic DNA extracted from *Bacillus* sp. strain KSM-S237 (FERM BP-7875) by a routine method, and using a primer set consisting of primers 237UB1 and Q58R-RV and a primer set consisting of primers Q58R-FW and S237RV indicated in the above Table 2-3. As a result, a 0.7-kb amplified DNA fragment which includes a nucleotide mutation introduced at the position corresponding to the amino acid residue at position 58 on the S237 cellulase gene (SEQ ID NO: 1) in the vicinity of the 3'-terminus and a region that is mainly in the upstream of the mutation position, and a 2.5-kb amplified DNA fragment which includes the nucleotide mutation in the vicinity of the 5'-terminus and a region that is mainly in the downstream of the mutation position, were obtained. The base sequence of the primer Q58R-RV thus used was designed based on the base sequence of the S237 cellulase gene, wherein the nucleotide mutation for substituting glutamine at position 58 of S237 cellulase with arginine is included. The base sequence of the primer Q58R-FW is a complementary sequence of the primer Q58R-RV.

Subsequently, the two fragments thus obtained were mixed to be used as templates, and SOE (splicing by Overlap Extension)-PCR (Horton R. M. et al., Gene (1989) 77(1), p. 61-68) was carried out according to the section "1) Amplification of DNA fragment", using a primer set consisting of 237UB1 and S237RV indicated in Table 1. Thus, a 3.2-kb DNA fragment in which those two fragments are linked through a complementary sequence was obtained.

## 54

The 3.2-kb DNA fragment thus obtained (mutant S237 cellulase gene) was inserted at the *Sma*I restriction enzyme cleavage point of a shuttle vector pHY300PLK, and thus a recombinant plasmid pHY-S237\_Q58R was constructed. The base sequence of the mutant S237 cellulase gene inserted in the plasmid was confirmed by determining the sequence using a 3100 DNA Sequencer (Applied Biosystems, Inc.). Subsequently, a transformant obtained by introducing the recombinant plasmid pHY-S237\_Q58R into *Bacillus subtilis* by the method according to the section "2) Gene introduction into *Bacillus subtilis*", was cultured. From the culture thus obtained, a recombinantly produced protein was isolated and purified by the same method as in the section "5) 1. Recombinant production of S237 cellulase", and quantification was carried out. This recombinant protein is a mutant S237 cellulase in which glutamine at position 58 of the amino acid sequence of S237 cellulase (SEQ ID NO: 2) has been substituted with arginine (hereinafter, also referred to as S237\_Q58R). An enzyme sample containing the mutant S237 cellulase thus obtained was used in the evaluation of antiredeposition ability in Test Example 1 described below.

## Example 2

## Production of Mutant S237 Cellulase-2

A mutant S237 cellulase, S237\_Q242S, in which glutamine at position 242 of S237 cellulase (SEQ ID NO: 2) was substituted with serine, was produced by the same method as described in Example 1. That is, the upstream region of the S237 cellulase gene (SEQ ID NO: 1) containing the intended nucleotide mutation (region in the upstream of the vicinity of the mutation position), and the downstream region of the S237 cellulase gene (SEQ ID NO: 1) containing the intended nucleotide mutation (region in the downstream of the vicinity of the mutation position) were amplified by PCR, using a primer set consisting of 237UB1 and Q242S-RV and a primer set consisting of Q242S-FW and S237RV indicated in Table 2-3. Two DNA fragments thus obtained were used as templates, and thus a 3.2-kb DNA fragment containing the intended mutant S237 cellulase gene was amplified. The DNA fragment was inserted into a shuttle vector pHY300PLK, and thus a recombinant plasmid pHY-S237\_Q242S was constructed. The base sequence of the mutant S237 cellulase gene inserted into the plasmid was confirmed, and a transformant obtained by introducing the recombinant plasmid into *Bacillus subtilis* by the method according to the section "2) Gene introduction into *Bacillus subtilis*" was cultured. A recombinant protein (that is, mutant S237 cellulase S237\_Q242S) was isolated and purified from the culture thus obtained, and quantification of the recombinant protein was carried out.

Based on this mutant S237 cellulase S237\_Q242S, two kinds of S237 cellulase double mutant, in which glutamine at position 58 was substituted with arginine or glutamic acid (QS\_Q58R and QS\_Q58E, respectively), were produced basically in the same manner as described in Example 1. First, two DNA fragments were obtained by performing PCR amplification of the upstream region (region in the upstream of the vicinity of the mutation position) of the mutant S237 cellulase S237\_Q242S gene containing the intended nucleotide mutation in the vicinity of the 3'-terminal, and the downstream region (region in the downstream of the vicinity of the mutation position) of the mutant S237 cellulase S237\_Q242S gene containing the intended nucleotide mutation, using the pHY-S237\_Q242S produced as described above as a template DNA, and respectively using two pairs of primer sets for



## 55

introducing the intended mutations indicated in the above Table 2-3. Using the two DNA fragments thus obtained as templates, a DNA fragment including the intended mutant S237 cellulase gene was amplified. The DNA fragment was inserted into a shuttle vector pHY300PLK to construct a recombinant plasmid, and the base sequence of the mutant S237 cellulase gene inserted in the plasmid was confirmed. A transformant obtained by introducing the recombinant plasmid into *Bacillus subtilis* by the method according to the section “2) Gene introduction into *Bacillus subtilis*”, was cultured. From the culture thus obtained, a recombinant protein (mutant S237 cellulase) was isolated and purified by the same method as in the section “5) 1. Recombinant production of S237 cellulase”, and quantification of the recombinant protein was carried out. Enzyme samples containing the respective mutant S237 cellulases thus obtained were used in an evaluation of the anti-redeposition ability and an evaluation of stability in Test Examples 2 and 3 described below.

## Example 3

## Production of Mutant S237 Cellulase-3

A mutant S237 cellulase in which serine at position 193 of S237 cellulase (SEQ ID NO: 2) was substituted with arginine, was produced by introducing a nucleotide mutation into the S237 cellulase gene, and recombinantly expressing the mutant, as follows.

PCR amplification was carried out according to the section “1) Amplification of DNA fragment”, using the genomic DNA extracted from *Bacillus* sp. strain KSM-S237 (FERM BP-7875) by a routine method as a template, and using a primer set consisting of primers 237UB1 and S193R-RV and a primer set consisting of primers S193R-FW and S237RV indicated in the above Table 2-1. As a result, a 0.7-kb amplified DNA fragment which includes a nucleotide mutation introduced at the position corresponding to the amino acid residue at position 193 on the S237 cellulase gene (SEQ ID NO: 1) in the vicinity of the 3'-terminus and a region that is mainly in the upstream of the mutation position, and a 2.5-kb amplified DNA fragment which includes the nucleotide mutation in the vicinity of the 5'-terminus and a region that is mainly in the downstream of the mutation position, were obtained. The base sequence of the primer S193R-RV thus used was designed based on the base sequence of S237 cellulase gene, wherein a nucleotide mutation for substituting serine at position 193 of S237 cellulase with arginine is included. The base sequence of the primer S193R-FW is a complementary sequence of the primer S193R-RV.

Subsequently, the two fragments thus obtained were mixed to be used as templates, and SOE (splicing by Overlap Extension)-PCR (Horton R. M. et al., *Gene* (1989) 77(1), p. 61-68) was carried out according to the section “1) Amplification of DNA fragment”, using a primer set consisting of 237UB1 and S237RV indicated in Table 1. Thus, a 3.2-kb DNA fragment in which those two fragments are linked through a complementary sequence was obtained.

The 3.2-kb DNA fragment thus obtained (mutant S237 cellulase gene) was inserted at the *Sma*I restriction enzyme cleavage point of a shuttle vector pHY300PLK, and thus a recombinant plasmid pHY-S237(S193R) was constructed. The base sequence of the mutant S237 cellulase gene inserted in the plasmid was confirmed by determining the sequence using a 3100 DNA Sequencer (Applied Biosystems, Inc.). Subsequently, a transformant obtained by introducing the recombinant plasmid pHY-S237(S193R) into *Bacillus subtilis* by the method according to the section “2) Gene introduc-

## 56

tion into *Bacillus subtilis*”, was cultured. From the culture thus obtained, a recombinantly produced protein was isolated and purified by the same method as in the section “5) 1. Recombinant production of S237 cellulase”, and quantification was carried out. This recombinant protein is a mutant S237 cellulase in which serine at position 193 of the amino acid sequence of S237 cellulase (SEQ ID NO: 2) had been substituted with arginine (hereinafter, also referred to as S237\_S193R). An enzyme sample containing the mutant S237 cellulase thus obtained, S237 S193R, was used in the evaluation of anti-redeposition ability in Test Example 4 described below.

## Example 4

## Production of Mutant S237 Cellulase-4

A mutant S237 cellulase in which the non-charged amino acid residues selected as described above were substituted with charged amino acid residues in the mutant S237 cellulase described in Example 2, S237\_Q242S, was produced. Specifically, a S237 cellulase double mutant (QS-Q71E) in which glutamine at position 71 of the amino acid sequence of the mutant S237 cellulase S237\_Q242S had been substituted with glutamic acid, was produced basically in the same manner as described in Example 3. First, two DNA fragments were obtained by performing PCR amplification of the upstream region (region in the upstream of the vicinity of the mutation position) of the mutant S237 cellulase S237\_Q242S gene containing the intended nucleotide mutation in the vicinity of the 3'-terminal, and the downstream region (region in the downstream of the vicinity of the mutation position) of the mutant S237 cellulase S237\_Q242S gene containing the intended nucleotide mutation, using the pHY-S237 (Q242S) produced as described above as a template DNA, and respectively using two pairs of primer sets for introducing the intended mutations indicated in the above Table 2-1. Using the two DNA fragments thus obtained as templates, a DNA fragment including the intended mutant S237 cellulase gene was amplified. That DNA fragment was inserted into a shuttle vector pHY300PLK to construct a recombinant plasmid, and the base sequence of the mutant S237 cellulase gene inserted in the plasmid was confirmed. A transformant obtained by introducing the recombinant plasmid into *Bacillus subtilis* by the method according to the section “2) Gene introduction into *Bacillus subtilis*”, was cultured. From the culture thus obtained, a recombinant protein (mutant S237 cellulase) was isolated and purified by the same method as in the section “5) 1. Recombinant production of S237 cellulase”, and quantification of the recombinant protein was carried out. Enzyme samples containing the respective mutant S237 cellulases thus obtained were used in an evaluation of the anti-redeposition ability and an evaluation of stability in Test Example 5 described below.

## Example 5

## Production of Mutant S237 Cellulase-5

Three kinds of mutant S237 cellulases, in which the amino acid residues participating in cellulose binding were substituted with introducing nucleotide mutations that cause intended amino acid substitutions into the S237 cellulase gene, and recombinantly expressing the mutants, were produced. Specifically, mutant S237 cellulases in which aspartic acid at position 421 of S237 cellulase (SEQ ID NO: 2) was substituted with alanine, tryptophan at position 454 substi-

tuted with tyrosine, and tryptophan at position 501 substituted with tyrosine (S237\_D421A, S237\_W454Y, and S237\_W501Y, respectively) were produced.

For each of the mutant cellulases, two DNA fragments were obtained by performing PCR amplification of the upstream region (region in the upstream of the vicinity of the mutation position) of the mutant S237 cellulase gene containing the intended nucleotide mutations, and the downstream region (region in the downstream of the vicinity of the mutation position) of the mutant S237 cellulase gene containing the intended nucleotide mutations, respectively using two pairs of primer sets for introducing the intended mutations (see Table 2-2). Using the two DNA fragments thus obtained as templates, a DNA fragment including the intended mutant S237 cellulase gene was amplified. That DNA fragment was inserted into a shuttle vector pHY300PLK to construct a recombinant plasmid, and the base sequence of the mutant S237 cellulase gene inserted in the plasmid was confirmed. A transformant obtained by introducing the recombinant plasmid into *Bacillus subtilis* by the method according to the section “2) Gene introduction into *Bacillus subtilis*”, was cultured. From the culture thus obtained, a recombinant protein (that is, each mutant S237 cellulase) was extracted and purified by the same method as in the section “5) 1. Recombinant production of S237 cellulase”, and quantification of the recombinant protein was carried out. Enzyme samples containing the respective mutant S237 cellulases thus obtained were used in an evaluation of the anti-redeposition ability in Test Example 6 described below.

Example 6

Production of Mutant S237 Cellulase-6

A mutant S237 cellulase, in which the amino acid residues participating in cellulose binding were further substituted in the mutant S237 cellulase S237\_Q242S described in Example 2, was produced. Specifically, a S237 cellulase double variant (QS\_N419A) in which asparagine at position 419 of the amino acid sequence of the mutant S237 cellulase S237\_Q242S was substituted with alanine, was produced basically in the same manner as described in Example 5. That is, two DNA fragments were obtained by performing PCR amplification of the upstream region (region in the upstream of the vicinity of the mutation position) of the mutant S237 cellulase S237\_Q242S gene containing the intended nucleotide mutation, and the downstream region (region in the downstream of the vicinity of the mutation position) of the mutant S237 cellulase S237\_Q242S gene containing the intended nucleotide mutation, using the pHY-S237(Q242S) produced as described above as a template DNA and respectively using two pairs of primer sets for introducing the intended mutations (see Table 2-2). Using the two DNA fragments thus obtained as templates, a DNA fragment including the intended mutant S237 cellulase gene was amplified. That DNA fragment was inserted into a shuttle vector pHY300PLK to construct a recombinant plasmid, and the base sequence of the mutant S237 cellulase gene inserted in the plasmid was confirmed. A transformant obtained by introducing the recombinant plasmid into *Bacillus subtilis* by the method according to the section “2) Gene introduction into *Bacillus subtilis*”, was cultured. From the culture thus obtained, a recombinant protein (that is, each mutant S237 cellulase) was isolated and purified by the same method as in the section “5) 1. Recombinant production of S237 cellulase”, and quantification of the recombinant protein was carried out. Enzyme samples containing the respective mutant

S237 cellulases thus obtained were used in an evaluation of the anti-redeposition ability in Test Example 7 described below.

Test Example 1

Evaluation of Anti-Redeposition Ability of Mutant S237 Cellulase-1

The anti-redeposition ability of mutant S237 cellulase S237\_Q58R produced in Example 1 was evaluated according to the section “4) Evaluation of anti-redeposition ability” described above. Furthermore, for the evaluation, 50 g of a white knitted cotton cloth [seared bleached cloth (supplied by Tanigashira Shoten) that had been washed and then sufficiently rinsed] was introduced, such that the amount of cloth with respect to the solution (bath ratio) would be 10 L/kg. The detergent composition B described above was used, and an amount of enzyme equivalent to the amount of protein exhibiting 52.8 mU of the wild-type S237 cellulase activity with respect to the S237\_Q58R, was used. The results obtained are shown in Table 7. Enhanced anti-redeposition ability of the mutant S237 cellulase S237\_Q58R as compared with S237 cellulase was observed.

TABLE 7

Enzyme	Effect of mutation on anti-redeposition (%)
Control	0
S237_Q58R	2.77

Test Example 2

Evaluation of Anti-Redeposition Ability of Mutant S237 Cellulase-2

The anti-redeposition ability of the mutant S237 cellulases QS\_Q58R and QS\_Q58E that had been produced in Example 2 using S237\_Q242S as the parent cellulase, was evaluated according to the section “4) Evaluation of anti-redeposition ability” described above. Furthermore, upon the evaluation, assuming the co-presence of sebum dirt components, three sheets of a stained cloth wfk10D (Wfk Testgewebe GmbH (D41379, Germany)) each having a size of 6 cm×6 cm were added. A cleaning agent of the composition C was used, and an amount of enzyme equivalent to the amount of protein exhibiting 52.8 mU of the S237\_Q242S cellulase activity was used. In the present evaluation, S237\_Q242S was used as a control enzyme. The results thus obtained are presented in Table 8. For any of the mutant S237 cellulases evaluated and used, a high anti-redeposition effect was obtained as compared with the control enzyme (S237\_Q242S), and the enhanced anti-redeposition ability by mutagenesis was observed.

TABLE 8

Enzyme	Effect of mutation on anti-redeposition (%)
Control	0
QS_Q58E	3.03
Control	0
QS_Q58R	8.92

## Test Example 3

## Stability Test of Mutant S237 Cellulase in Liquid Cleaning Agent

Stability was evaluated for the case where the mutant S237 cellulase QS\_Q58R produced by using S237\_Q242S as a parent cellulase in Example 3 was stored in a cleaning agent of the composition E to which various alkaline proteases were added.

As the alkaline proteases, alkaline proteases KP43 (Japanese Patent No. 3479509), Kannase™ (Novozymes, Inc.) and Properase™ (Danisco AS) were used. These three kinds of alkaline proteases are all subtilisin-like alkaline proteases suitable to be incorporated into cleaning agents.

To 450  $\mu$ L of the cleaning agent of the composition E, 460 U/L of a cellulase (S237QS or S237QS\_Q58R) and 0.012 g each, as an amount of protein, of the three kinds of alkaline proteases described above (an amount of protein equivalent to the addition of 29 U/L for KP43) were added, and liquid amount of the samples were adjusted to 500  $\mu$ L, and were stored at 40° C. The residual cellulase activity in the cleaning agent after 24 hours was measured.

The cellulase activity was measured by the method of using p-nitrophenyl- $\beta$ -D-cellobioside described in Example 1, and the residual cellulase activity was calculated by the following formula.

$$\text{Residual cellulase activity (\%)} = \frac{\text{Cellulase activity after 24 hours of storage}}{\text{cellulase activity immediately after preparation}} \times 100 \quad [\text{Mathematical formula 8}]$$

The experimental results are presented in FIG. 4. The relative residual activity of QS\_Q58R is shown by defining the residual activity value of S237\_QS after storage for 24 hours at 40° C. as 100. For all of the systems to which the three kinds of proteases were added, QS\_Q58R exhibited higher residual activity as compared with S237QS. From these results, enhancements of the anti-redeposition ability and the protease resistance by substituting glutamine at position 58 of S237 cellulase with arginine were observed.

## Test Example 4

## Evaluation of Anti-Redeposition Ability of Mutant S237 Cellulase-3

The anti-redeposition ability of the mutant S237 cellulase S237\_S193R produced in Example 3 was evaluated according to the section “4) Evaluation of anti-redeposition ability” described above. Furthermore, for the evaluation, 50 g of a white knitted cotton cloth [seared bleached cloth (supplied by Tanigashira Shoten) that had been washed and then sufficiently rinsed] was introduced, such that the amount of cloth with respect to the solution (bath ratio) would be 10 L/kg. A cleaning agent of the composition F described above was used, and an amount of enzyme equivalent to the amount of protein exhibiting 52.8 mU of the wild-type S237 cellulase activity with respect to the S237\_S193R, was used. Asahi carbon black for cleaning was used as the carbon black, and the hardness of the used water was adjusted to 12° DH. The results thus obtained are shown in Table 9. Furthermore, the value of solvent accessibility determined in Example 2 is also presented. With S237\_S193R, a higher anti-redeposition effect as compared with the control enzyme (S237\_Q242S) was provided, and enhancement of the anti-redeposition ability by the mutagenesis was observed.

TABLE 9

Mutant S237 cellulase	Degree of anti-redeposition ability enhancement in mutant cellulase (%)	Solvent accessibility of residue at mutation position
S237_S193R	3.26	76.08

## Test Example 5

## Evaluation of Anti-Redeposition Ability of Mutant S237 Cellulase-4

The anti-redeposition ability of the mutant S237 cellulase QS\_Q71E produced in Example 4 using S237\_Q242S as a base, was evaluated according to the section “4) Evaluation of anti-redeposition ability” described above.

A cleaning agent of the composition C described above was used, and an amount of enzyme equivalent to the amount of protein exhibiting 52.8 mU of the wild-type S237 cellulase activity with respect to QS\_Q71E, was used. For the present evaluation, S237\_Q242S was used as a control enzyme. Asahi carbon black for cleaning was used as the carbon black, and the hardness of the used water was adjusted to 4° DH. Furthermore, upon the evaluation, assuming the co-presence of sebum dirt components, three sheets of a stained cloth wfk10D (Wfk Testgewebe GmbH (D41379, Germany)) each having a size of 6 cm $\times$ 6 cm were added. The results thus obtained are shown in Table 10. Further, the value of the solvent accessibility of residues determined in the section “6) Steric structure modeling of S237 cellulase” described above is also shown. Higher anti-redeposition effect as compared with the control enzyme (S237\_Q242S) was provided in QS\_Q71E, and enhancement of the anti-redeposition ability by the mutagenesis was observed. From the results of the present Test Example and the Test Example 4, it was demonstrated that the anti-redeposition ability of the mutant S237 cellulases can be enhanced by substituting the non-charged amino acid residues selected as described above, with charged amino acid residues. The result suggests that such amino acid substitution caused high repulsion between the enzyme surface and hydrophobic carbon black by further increasing the hydrophilicity of the enzyme surface, as speculated in the above, and thereby a higher anti-redeposition effect was provided.

TABLE 10

Mutant S237 cellulase	Degree of anti-redeposition ability enhancement in mutant cellulase (%)	Solvent accessibility of residue at mutation position
QS_Q71E	6.06	116.3

## Test Example 6

## Evaluation of Anti-Redeposition Ability of Mutant S237 Cellulase-5

The anti-redeposition ability of the mutant S237 cellulases produced in Example 5, S237\_D421A, S237\_W454Y and S237\_W501Y, was evaluated according to the section “4) Evaluation of anti-redeposition ability” described above. For the evaluation, 50 g of a white knitted cotton cloth [seared bleached cloth (supplied by Tanigashira Shoten) that had been washed and then sufficiently rinsed] was introduced,

## 61

such that the amount of cloth with respect to the solution (bath ratio) would be 10 L/kg. A cleaning agent of the composition B described above was used, and an amount of enzyme equivalent to the amount of protein exhibiting 52.8 mU of the wild-type S237 cellulase activity with respect to each of the mutant S237 cellulases, was used. In the present evaluation, the wild-type S237 cellulase was used as a control enzyme. Asahi carbon black for cleaning was used as the carbon black, and the hardness of the used water was adjusted to 12° DH. The results thus obtained are shown in Table 11. For all of the mutant S237 cellulases, an enhancement of the anti-redeposition ability as compared with S237 cellulase was observed. Therefore, it was demonstrated that when the amino acid residues that participate in cellulose binding in the cellulose binding module of an alkaline cellulase are substituted with other amino acid residues, the anti-redeposition ability of a mutant S237 cellulase can be enhanced. The result suggests that such amino acid substitution decreased the cellulose binding property of the alkaline cellulase as speculated in the above, and thereby a higher anti-redeposition effect was provided.

TABLE 11

Mutant S237 cellulase	Degree of anti-redeposition ability enhancement in mutant cellulase (%)
S237_D421A	3.29
S237_W454Y	4.21
S237_W501Y	10.5

## Test Example 7

## Evaluation of Anti-Redeposition Ability of Mutant S237 Cellulase-6

The anti-redeposition ability of the mutant S237 cellulase QS\_N419A produced in Example 6 using S237\_Q242S as a

## 62

base, was evaluated according to the section “4) Evaluation of anti-redeposition ability” described above. For the evaluation, 45 g of a white knitted cotton cloth [seared bleached cloth (supplied by Tanigashira Shoten) that had been washed and then sufficiently rinsed] was introduced, such that the amount of cloth with respect to the solution (bath ratio) would be 11 L/kg. A cleaning agent of the composition C described above was used, and an amount of enzyme equivalent to the amount of protein exhibiting 52.8 mU of the wild-type S237 cellulase activity with respect to QS\_N419A, was used. In the present evaluation, S237\_Q242S was used as a control enzyme. Asahi carbon black for cleaning was used as the carbon black, and the hardness of the used water was adjusted to 4° DH. Furthermore, upon the evaluation, assuming the co-presence of sebum dirt components, three sheets of a stained cloth wfk10D (Wfk Testgewebe GmbH (D41379, Germany)) each having a size of 6 cm×6 cm were added. The results thus obtained are shown in Table 12. Higher anti-redeposition effect as compared with the control enzyme (S237\_Q242S) was provided in QS\_N419A, and enhancement of the anti-redeposition ability by the mutagenesis was observed. That is, it was demonstrated that when the amino acid residues that participate in cellulose binding in the cellulose binding module of an alkaline cellulase are substituted with other amino acid residues, the anti-redeposition ability of a mutant S237 cellulase can be enhanced. The result suggests that such amino acid substitution decreased the cellulose binding property of the alkaline cellulase as speculated in the above, and thereby a higher anti-redeposition effect was provided.

TABLE 12

Mutant S237 cellulase	Degree of anti-redeposition ability enhancement in mutant cellulase (%)
QS_N419A	4.62

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Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly  
65 70 75 80

Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn

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85								90					95				
Ala	Tyr	Lys	Ala	Leu	Ser	Asn	Asp	Trp	Asp	Ser	Asn	Met	Ile	Arg	Leu		
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Ala	Met	Tyr	Val	Gly	Glu	Asn	Gly	Tyr	Ala	Thr	Asn	Pro	Glu	Leu	Ile		
		115					120					125					
Lys	Gln	Arg	Val	Ile	Asp	Gly	Ile	Glu	Leu	Ala	Ile	Glu	Asn	Asp	Met		
	130					135					140						
Tyr	Val	Ile	Val	Asp	Trp	His	Val	His	Ala	Pro	Gly	Asp	Pro	Arg	Asp		
145				150						155					160		
Pro	Val	Tyr	Ala	Gly	Ala	Lys	Asp	Phe	Phe	Arg	Glu	Ile	Ala	Ala	Leu		
			165					170						175			
Tyr	Pro	Asn	Asn	Pro	His	Ile	Ile	Tyr	Glu	Leu	Ala	Asn	Glu	Pro	Ser		
		180						185					190				
Ser	Asn	Asn	Asn	Gly	Gly	Ala	Gly	Ile	Pro	Asn	Asn	Glu	Glu	Gly	Trp		
	195						200					205					
Lys	Ala	Val	Lys	Glu	Tyr	Ala	Asp	Pro	Ile	Val	Glu	Met	Leu	Arg	Lys		
	210					215					220						
Ser	Gly	Asn	Ala	Asp	Asp	Asn	Ile	Ile	Ile	Val	Gly	Ser	Pro	Asn	Trp		
225				230						235					240		
Ser	Gln	Arg	Pro	Asp	Leu	Ala	Ala	Asp	Asn	Pro	Ile	Asp	Asp	His	His		
			245					250						255			
Thr	Met	Tyr	Thr	Val	His	Phe	Tyr	Thr	Gly	Ser	His	Ala	Ala	Ser	Thr		
		260						265						270			
Glu	Ser	Tyr	Pro	Ser	Glu	Thr	Pro	Asn	Ser	Glu	Arg	Gly	Asn	Val	Met		
	275						280					285					
Ser	Asn	Thr	Arg	Tyr	Ala	Leu	Glu	Asn	Gly	Val	Ala	Val	Phe	Ala	Thr		
	290					295				300							
Glu	Trp	Gly	Thr	Ser	Gln	Ala	Ser	Gly	Asp	Gly	Gly	Pro	Tyr	Phe	Asp		
305				310					315						320		
Glu	Ala	Asp	Val	Trp	Ile	Glu	Phe	Leu	Asn	Glu	Asn	Asn	Ile	Ser	Trp		
		325						330						335			
Ala	Asn	Trp	Ser	Leu	Thr	Asn	Lys	Asn	Glu	Val	Ser	Gly	Ala	Phe	Thr		
		340					345						350				
Pro	Phe	Glu	Leu	Gly	Lys	Ser	Asn	Ala	Thr	Asn	Leu	Asp	Pro	Gly	Pro		
	355						360					365					
Asp	His	Val	Trp	Ala	Pro	Glu	Glu	Leu	Ser	Leu	Ser	Gly	Glu	Tyr	Val		
	370					375					380						
Arg	Ala	Arg	Ile	Lys	Gly	Val	Asn	Tyr	Glu	Pro	Ile	Asp	Arg	Thr	Lys		
385				390						395					400		
Tyr	Thr	Lys	Val	Leu	Trp	Asp	Phe	Asn	Asp	Gly	Thr	Lys	Gln	Gly	Phe		
		405						410						415			
Gly	Val	Asn	Ser	Asp	Ser	Pro	Asn	Lys	Glu	Leu	Ile	Ala	Val	Asp	Asn		
		420						425					430				
Glu	Asn	Asn	Thr	Leu	Lys	Val	Ser	Gly	Leu	Asp	Val	Ser	Asn	Asp	Val		
	435						440					445					
Ser	Asp	Gly	Asn	Phe	Trp	Ala	Asn	Ala	Arg	Leu	Ser	Ala	Asn	Gly	Trp		
	450					455					460						
Gly	Lys	Ser	Val	Asp	Ile	Leu	Gly	Ala	Glu	Lys	Leu	Thr	Met	Asp	Val		
465				470					475						480		
Ile	Val	Asp	Glu	Pro	Thr	Thr	Val	Ala	Ile	Ala	Ala	Ile	Pro	Gln	Ser		
			485					490						495			
Ser	Lys	Ser	Gly	Trp	Ala	Asn	Pro	Glu	Arg	Ala	Val	Arg	Val	Asn	Ala		
			500					505					510				



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Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala Gly Leu Thr  
 515 520 525  
 Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala Phe His Glu  
 530 535 540  
 Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly Thr Asp Ala  
 545 550 555 560  
 Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val  
 565 570 575  
 Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser  
 580 585 590  
 Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser  
 595 600 605  
 Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala  
 610 615 620  
 Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp  
 625 630 635 640  
 Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly  
 645 650 655  
 Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala  
 660 665 670  
 Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn  
 675 680 685  
 Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu  
 690 695 700  
 Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys  
 705 710 715 720  
 Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg  
 725 730 735  
 Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg  
 740 745 750  
 Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro  
 755 760 765  
 Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp  
 770 775 780  
 Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys  
 785 790 795 800  
 Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala  
 805 810 815  
 Val Lys Asn Glu Ala Lys Lys Lys  
 820

<210> SEQ ID NO 3  
 <211> LENGTH: 2322  
 <212> TYPE: DNA  
 <213> ORGANISM: Bacillus sp. strain DSM12648  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(2319)

<400> SEQUENCE: 3

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1 5 10 15	
gac aat gtt aaa cgc cct tct gag gct ggc gca tta caa tta caa gaa	96
Asp Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu	
20 25 30	

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gtc gat gga caa atg aca tta gta gat caa cat gga gaa aaa att caa Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln 35 40 45	144
tta cgt gga atg agt aca cac gga tta caa tgg ttt cct gar atc ttg Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu 50 55 60	192
aat gat aac gca tac aaa gct ctt gct aac gat tgg gaa tca aat atg Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met 65 70 75 80	240
att cgt cta gct atg tat gtc ggt gaa aat ggc tat gct tca aat cca Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro 85 90 95	288
gag tta att aaa agc aga gtc att aaa gga ata gat ctt gct att gaa Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu 100 105 110	336
aat gac atg tat gtt att gtt gat tgg cat gta cat gca cct ggt gat Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp 115 120 125	384
cct aga gat ccc gtt tac gct gga gca gaa gat ttc ttt aga gat att Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile 130 135 140	432
gca gca tta tat cct aac aat cca cac att att tat gag tta gcg aat Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn 145 150 155 160	480
gag cca agt agt aac aat aat ggt gga gct ggg att cca aat aat gaa Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu 165 170 175	528
gaa ggt tgg aat gcg gta aaa gaa tac gct gat cca att gta gaa atg Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met 180 185 190	576
tta cgt gat agc ggg aac gca gat gac aat atc atc att gtg ggt agt Leu Arg Asp Ser Gly Asn Ala Asp Asn Ile Ile Ile Val Gly Ser 195 200 205	624
cca aac tgg agt cag cgt cct gac tta gca gct gat aat cca att aat Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asn 210 215 220	672
gat cac cat aca atg tat act gtt cac ttc tac act ggt tca cat gct Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala 225 230 235 240	720
gct tca act gag agc tat ccg cct gaa act cct aac tct gaa aga gga Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly 245 250 255	768
aac gta atg agt aac act cgt tat gcg tta gaa aac gga gta gcg gta Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val 260 265 270	816
ttt gcg aca gaa tgg gga aca agt caa gca aat gga gat ggt ggt cct Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro 275 280 285	864
tat ttt gat gaa gca gat gta tgg att gag ttt tta aat gaa aac aac Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn 290 295 300	912
att agt tgg gct aac tgg tct tta acg aat aaa aat gaa gtg tct ggt Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly 305 310 315 320	960
gca ttt aca cca ttc gag tta ggt aag tct aac gca acc aat ctt gac Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp 325 330 335	1008
cca ggt cca gat cat gtg tgg gca cca gaa gag tta agt ctt tcg gga Pro Gly Pro Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly	1056

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340	345	350	
gaa tat gta cgt gct cgt att aaa ggt gtg aac tat gag cca atc gac Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp 355 360 365			1104
cgt aca aaa tac acg aaa gta ctt tgg gac ttt aat gat gga acg aag Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys 370 375 380			1152
caa gga ttt gga gtg aat tcg gat tct cca aat aaa gaa ctt att gca Gln Gly Phe Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala 385 390 395 400			1200
gtt gat aat gaa aac aac act ttg aaa gtt tcg gga tta gat gta agt Val Asp Asn Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser 405 410 415			1248
aac gat gtt tca gat ggc aac ttc tgg gct aat gct cgt ctt tct gcc Asn Asp Val Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala 420 425 430			1296
gac ggt tgg gga aaa agt gtt gat att tta ggt gct gag aag ctt aca Asp Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr 435 440 445			1344
atg gat gtt att gtt gat gaa cca acg acg gta gct att gcg gcg att Met Asp Val Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile 450 455 460			1392
cca caa agt agt aaa agt gga tgg gca aat cca gag cgt gct gtt cga Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg 465 470 475 480			1440
gtg aac gcg gaa gat ttt gtt cag caa acg gac ggt aag tat aaa gct Val Asn Ala Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala 485 490 495			1488
gga tta aca att aca gga gaa gat gct cct aac cta aaa aat atc gct Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala 500 505 510			1536
ttt cat gaa gaa gat aac aat atg aac aac atc att ctg ttc gtg gga Phe His Glu Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly 515 520 525			1584
act gat gca gct gac gtt att tac tta gat aac att aaa gta att gga Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly 530 535 540			1632
aca gaa gtt gaa att cca gtt gtt cat gat cca aaa gga gaa gct gtt Thr Glu Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val 545 550 555 560			1680
ctt cct tct gtt ttt gaa gac ggt aca cgt caa ggt tgg gac tgg gct Leu Pro Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala 565 570 575			1728
gga gag tct ggt gtg aaa aca gct tta aca att gaa gaa gca aac ggt Gly Glu Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly 580 585 590			1776
tct aac gcg tta tca tgg gaa ttt gga tat cca gaa gta aaa cct agt Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser 595 600 605			1824
gat aac tgg gca aca gct cca cgt tta gat ttc tgg aaa tct gac ttg Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu 610 615 620			1872
gtt cgc ggt gag aat gat tat gta gct ttt gat ttc tat cta gat cca Val Arg Gly Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro 625 630 635 640			1920
gtt cgt gca aca gaa ggc gca atg aat atc aat tta gta ttc cag cca Val Arg Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro 645 650 655			1968
cct act aac ggg tat tgg gta caa gca cca aaa acg tat acg att aac			2016

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Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn	
660 665 670	
ttt gat gaa tta gag gaa gcg aat caa gta aat ggt tta tat cac tat	2064
Phe Asp Glu Leu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr	
675 680 685	
gaa gtg aaa att aac gta aga gat att aca aac att caa gat gac acg	2112
Glu Val Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr	
690 695 700	
tta cta cgt aac atg atg atc att ttt gca gat gta gaa agt gac ttt	2160
Leu Leu Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe	
705 710 715 720	
gca ggg aga gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act	2208
Ala Gly Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr	
725 730 735	
act gag cgt gtt gaa cca gag cca gtt gat cct ggc gaa gag acg cca	2256
Thr Glu Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro	
740 745 750	
cct gtc gat gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa	2304
Pro Val Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys	
755 760 765	
gaa gag aaa gaa gag taa	2322
Glu Glu Lys Glu Glu	
770	

&lt;210&gt; SEQ ID NO 4

&lt;211&gt; LENGTH: 773

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Bacillus sp. strain DSM12648

&lt;400&gt; SEQUENCE: 4

Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn	
1 5 10 15	
Asp Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu	
20 25 30	
Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln	
35 40 45	
Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu	
50 55 60	
Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met	
65 70 75 80	
Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro	
85 90 95	
Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu	
100 105 110	
Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp	
115 120 125	
Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile	
130 135 140	
Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn	
145 150 155 160	
Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu	
165 170 175	
Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met	
180 185 190	
Leu Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser	
195 200 205	
Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asn	

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210	215	220
Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala		
225	230	235 240
Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly		
	245	250 255
Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val		
	260	265 270
Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro		
	275	280 285
Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn		
	290	295 300
Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly		
	305	310 315 320
Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp		
	325	330 335
Pro Gly Pro Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly		
	340	345 350
Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp		
	355	360 365
Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys		
	370	375 380
Gln Gly Phe Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala		
	385	390 395 400
Val Asp Asn Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser		
	405	410 415
Asn Asp Val Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala		
	420	425 430
Asp Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr		
	435	440 445
Met Asp Val Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile		
	450	455 460
Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg		
	465	470 475 480
Val Asn Ala Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala		
	485	490 495
Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala		
	500	505 510
Phe His Glu Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly		
	515	520 525
Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly		
	530	535 540
Thr Glu Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val		
	545	550 555 560
Leu Pro Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala		
	565	570 575
Gly Glu Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly		
	580	585 590
Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser		
	595	600 605
Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu		
	610	615 620
Val Arg Gly Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro		
	625	630 635 640

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Val Arg Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro  
645 650 655

Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn  
660 665 670

Phe Asp Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr  
675 680 685

Glu Val Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr  
690 695 700

Leu Leu Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe  
705 710 715 720

Ala Gly Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr  
725 730 735

Thr Glu Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro  
740 745 750

Pro Val Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys  
755 760 765

Glu Glu Lys Glu Glu  
770

<210> SEQ ID NO 5  
 <211> LENGTH: 2923  
 <212> TYPE: DNA  
 <213> ORGANISM: Bacillus sp. strain 1139  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (203)..(2602)

<400> SEQUENCE: 5

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ttagataact tataagtgtg tgagaagcag gagagaatct gggttactca caagtttttt	120
aaaacattat cgaaagcact ttccggttatg cttatgaatt tagctatttg attcaattac	180
tttaataatt ttaggaggta at atg atg tta aga aag aaa aca aag cag ttg	232
Met Met Leu Arg Lys Lys Thr Lys Gln Leu	
1 5 10	
att tct tcc att ctt att tta gtt tta ctt cta tct tta ttt ccg aca	280
Ile Ser Ser Ile Leu Ile Leu Val Leu Leu Ser Leu Phe Pro Thr	
15 20 25	
gct ctt gca gca gaa gga aac act cgt gaa gac aat ttt aaa cat tta	328
Ala Leu Ala Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu	
30 35 40	
tta ggt aat gac aat gtt aaa cgc cct tct gag gct ggc gca tta caa	376
Leu Gly Asn Asp Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln	
45 50 55	
tta caa gaa gtc gat gga caa atg aca tta gta gat caa cat gga gaa	424
Leu Gln Glu Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu	
60 65 70	
aaa att caa tta cgt gga atg agt aca cac gga tta caa tgg ttt cct	472
Lys Ile Gln Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro	
75 80 85 90	
gag atc ttg aat gat aac gca tac aaa gct ctt gct aac gat tgg gaa	520
Glu Ile Leu Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu	
95 100 105	
tca aat atg att cgt cta gct atg tat gtc ggt gaa aat ggc tat gct	568
Ser Asn Met Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala	
110 115 120	
tca aat cca gag tta att aaa agc aga gtc att aaa gga ata gat ctt	616
Ser Asn Pro Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu	

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125	130	135	
gct att gaa aat gac atg Ala Ile Glu Asn Asp Met 140	tat gtc atc gtt gat Tyr Val Ile Val Asp 145	tgg cat gta cat gca Trp His Val His Ala 150	664
cct ggt gat cct aga gat Pro Gly Asp Pro Arg Asp 155	ccc gtt tac gct gga Pro Val Tyr Ala Gly 160	gca gaa gat ttc ttt Ala Glu Asp Phe Phe 165	712
aga gat att gca gca tta Arg Asp Ile Ala Ala Leu 175	tat cct aac aat cca Tyr Pro Asn Asn Pro 180	cac att att tat gag His Ile Ile Tyr Glu 185	760
tta gcg aat gag cca agt Leu Ala Asn Glu Pro Ser 190	agt aac aat aat ggt Ser Asn Asn Asn Gly 195	gga gct ggg att cca Gly Gly Ala Gly Ile Pro 200	808
aat aat gaa gaa ggt tgg Asn Asn Glu Glu Gly Trp 205	aat gcg gta aaa gaa Asn Ala Val Lys Glu 210	tac gct gat cca att Tyr Ala Asp Pro Ile 215	856
gta gaa atg tta cgt gat Val Glu Met Leu Arg Asp 220	agc ggg aac gca gat Ser Gly Asn Ala Asp 225	gac aat att atc att Asp Asn Ile Ile Ile 230	904
gtg ggt agt cca aac tgg Val Gly Ser Pro Asn Trp 235	agt cag cgt cct gac Ser Gln Arg Pro Asp 240	tta gca gct gat aat Leu Ala Ala Asp Asn 245	952
cca att gat gat cac cat Pro Ile Asp Asp His His 255	aca atg tat act gtt Thr Met Tyr Thr Val 260	cac ttc tac act ggt His Phe Tyr Thr Gly 265	1000
tca cat gct gct tca act Ser His Ala Ala Ser Thr 270	gaa agc tat ccg cct Glu Ser Tyr Pro Pro 275	gaa act cct aac tct Glu Thr Pro Asn Ser 280	1048
gaa aga gga aac gta atg Glu Arg Gly Asn Val Met 285	agt aac act cgt tat Ser Asn Thr Arg Tyr 290	gcg tta gaa aac gga Ala Leu Glu Asn Gly 295	1096
gta gca gta ttt gca aca Val Ala Val Phe Ala Thr 300	gag tgg gga act agc Glu Trp Gly Thr Ser 305	caa gca aat gga gat Gln Ala Asn Gly Asp 310	1144
ggt ggt cct tac ttt gat Gly Gly Pro Tyr Phe Asp 315	gaa gca gat gta tgg Glu Ala Asp Val Trp 320	att gag ttt tta aat Ile Glu Phe Leu Asn 325	1192
gaa aac aac att agc tgg Glu Asn Asn Ile Ser Trp 335	gct aac tgg tct tta Ala Asn Trp Ser Leu 340	acg aat aaa aat gaa Thr Asn Lys Asn Glu 345	1240
gta tct ggt gca ttt aca Val Ser Gly Ala Phe Thr 350	cca ttc gag tta ggt Pro Phe Glu Leu Gly 355	aag tct aac gca aca Lys Ser Asn Ala Thr 360	1288
agt ctt gac cca ggg cca Ser Leu Asp Pro Gly Pro 365	gac caa gta tgg gta Asp Gln Val Trp Val 370	cca gaa gag tta agt Pro Glu Glu Leu Ser 375	1336
ctt tct gga gaa tat gta Leu Ser Gly Glu Tyr Val 380	cgt gct cgt att aaa Ala Arg Ile Lys Gly 385	ggt gtg aac tat gag Val Asn Tyr Tyr Glu 390	1384
cca atc gac cgt aca aaa Pro Ile Asp Arg Thr Lys 395	tac acg aaa gta ctt Tyr Thr Lys Val Leu 400	tgg gac ttt aat gat Trp Asp Phe Asn Asp 405	1432
gga acg aag caa gga ttt Gly Thr Lys Gln Gly Phe 415	gga gtg aat gga gat Gly Val Asn Gly Asp 420	tct cca gtt gaa gat Ser Pro Val Glu Asp 425	1480
gta gtt att gag aat gaa Val Val Ile Glu Asn Glu 430	gcg ggc gct tta aaa Ala Gly Ala Leu Lys 435	ctt tca gga tta gat Leu Ser Gly Leu Asp 440	1528
gca agt aat gat gtt tct gaa ggt aat tac tgg gct aat gct cgt ctt			1576

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Ser	Ala	Asp	Gly	Trp	Gly	Lys	Ser	Val	Asp	Ile	Leu	Gly	Ala	Glu	Lys	
	460					465					470					
ctt	act	atg	gat	gtg	att	ggt	gat	gag	ccg	acc	acg	gta	tca	att	gct	1672
Leu	Thr	Met	Asp	Val	Ile	Val	Asp	Glu	Pro	Thr	Thr	Val	Ser	Ile	Ala	
475					480					485					490	
gca	att	cca	caa	ggg	cca	tca	gcc	aat	tgg	ggt	aat	cca	aat	cgt	gca	1720
Ala	Ile	Pro	Gln	Pro	Ser	Ala	Asn	Trp	Val	Asn	Pro	Asn	Arg	Ala		
			495					500					505			
att	aag	ggt	gag	cca	act	aat	ttc	gta	ccg	tta	gag	gat	aag	ttt	aaa	1768
Ile	Lys	Val	Glu	Pro	Thr	Asn	Phe	Val	Pro	Leu	Glu	Asp	Lys	Phe	Lys	
		510						515					520			
gcg	gaa	tta	act	ata	act	tca	gct	gac	tct	cca	tcg	tta	gaa	gct	att	1816
Ala	Glu	Leu	Thr	Ile	Thr	Ser	Ala	Asp	Ser	Pro	Ser	Leu	Glu	Ala	Ile	
	525						530						535			
gcg	atg	cat	gct	gaa	aat	aac	aac	atc	aac	atc	att	ctt	ttt	gta		1864
Ala	Met	His	Ala	Glu	Asn	Asn	Asn	Ile	Asn	Asn	Ile	Ile	Leu	Phe	Val	
	540					545				550						
gga	act	gaa	ggg	gct	gat	ggt	atc	tat	tta	gat	aac	att	aaa	gta	att	1912
Gly	Thr	Glu	Gly	Ala	Asp	Val	Ile	Tyr	Leu	Asp	Asn	Ile	Lys	Val	Ile	
555					560					565					570	
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Val	Leu	Pro	Ser	Val	Phe	Glu	Asp	Gly	Thr	Arg	Gln	Gly	Trp	Asp	Trp	
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gct	gga	gag	tct	ggg	gtg	aaa	aca	gct	tta	aca	att	gaa	gaa	gca	aac	2056
Ala	Gly	Glu	Ser	Gly	Val	Lys	Thr	Ala	Leu	Thr	Ile	Glu	Glu	Ala	Asn	
	605					610					615					
ggt	tct	aac	gcg	tta	tca	tgg	gaa	ttt	gga	tac	cca	gaa	gta	aaa	cct	2104
Gly	Ser	Asn	Ala	Leu	Ser	Trp	Glu	Phe	Gly	Tyr	Pro	Glu	Val	Lys	Pro	
	620					625					630					
agt	gat	aac	tgg	gca	aca	gct	cca	cgt	tta	gat	ttc	tgg	aaa	tct	gac	2152
Ser	Asp	Asn	Trp	Ala	Thr	Ala	Pro	Arg	Leu	Asp	Phe	Trp	Lys	Ser	Asp	
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Leu	Val	Arg	Gly	Glu	Asn	Asp	Tyr	Val	Thr	Phe	Asp	Phe	Tyr	Leu	Asp	
			655						660					665		
cca	ggt	cgt	gca	aca	gaa	ggc	gca	atg	aat	atc	aat	tta	gta	ttc	cag	2248
Pro	Val	Arg	Ala	Thr	Glu	Gly	Ala	Met	Asn	Ile	Asn	Leu	Val	Phe	Gln	
			670					675					680			
cca	cct	act	aac	ggg	tat	tgg	gta	caa	gca	cca	aaa	acg	tat	acg	att	2296
Pro	Pro	Thr	Asn	Gly	Tyr	Trp	Val	Gln	Ala	Pro	Lys	Thr	Tyr	Thr	Ile	
		685						690					695			
aac	ttt	gat	gaa	tta	gag	gaa	ccg	aat	caa	gta	aat	ggg	tta	tat	cac	2344
Asn	Phe	Asp	Glu	Leu	Glu	Glu	Pro	Asn	Gln	Val	Asn	Gly	Leu	Tyr	His	
	700					705					710					
tat	gaa	gtg	aaa	att	aac	gta	aga	gat	att	aca	aac	att	caa	gat	gac	2392
Tyr	Glu	Val	Lys	Ile	Asn	Val	Arg	Asp	Ile	Thr	Asn	Ile	Gln	Asp	Asp	
	715				720					725					730	
acg	tta	cta	cgt	aac	atg	atg	atc	att	ttt	gca	gat	gta	gaa	agt	gac	2440
Thr	Leu	Leu	Arg	Asn	Met	Met	Ile	Ile	Phe	Ala	Asp	Val	Glu	Ser	Asp	
			735						740					745		
ttt	gca	ggg	aga	gtc	ttt	gta	gat	aat	ggt	cgt	ttt	gag	ggg	gct	gct	2488
Phe	Ala	Gly	Arg	Val	Phe	Val	Asp	Asn	Val	Arg	Phe	Glu	Gly	Ala	Ala	
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act act gag ccg gtt gaa cca gag cca gtt gat cct ggc gaa gag acg	2536
Thr Thr Glu Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr	
765 770 775	
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Pro Pro Val Asp Glu Lys Glu Ala Lys Thr Glu Gln Lys Glu Ala Glu	
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aaa gaa gag aaa gaa gag taaagaaga aaagaagaa gctaaagaag	2632
Lys Glu Glu Lys Glu	
795 800	
aaaagaaagc aatcaaaaat gaggctacga aaaaataatc taataaacta gttatagggt	2692
tatctaaagg tctgatgcag atctttttaga taaccttttt ttgcataact ggacatagaa	2752
tggtttattaa agaaagcacg gtgttttatac gatattaaaa ggtagcgatt ttaattgaaa	2812
cctttaataa tgctcgtgtga tagaatgatg aagtaattta agagggggga aacgaagtga	2872
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&lt;211&gt; LENGTH: 800

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Bacillus sp. strain 1139

&lt;400&gt; SEQUENCE: 6

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Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val	
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Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly	
50 55 60	
Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly	
65 70 75 80	
Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn	
85 90 95	
Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met Ile Arg Leu	
100 105 110	
Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro Glu Leu Ile	
115 120 125	
Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu Asn Asp Met	
130 135 140	
Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp	
145 150 155 160	
Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile Ala Ala Leu	
165 170 175	
Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser	
180 185 190	
Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp	
195 200 205	
Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Asp	
210 215 220	
Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp	
225 230 235 240	
Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His	
245 250 255	
Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr	

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Ser	Asn	Thr	Arg	Tyr	Ala	Leu	Glu	Asn	Gly	Val	Ala	Val	Phe	Ala	Thr	
290								295								
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305								310		315						
Glu	Ala	Asp	Val	Trp	Ile	Glu	Phe	Leu	Asn	Glu	Asn	Asn	Ile	Ser	Trp	
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Ala	Asn	Trp	Ser	Leu	Thr	Asn	Lys	Asn	Glu	Val	Ser	Gly	Ala	Phe	Thr	
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Pro	Phe	Glu	Leu	Gly	Lys	Ser	Asn	Ala	Thr	Ser	Leu	Asp	Pro	Gly	Pro	
355								360								
Asp	Gln	Val	Trp	Val	Pro	Glu	Glu	Leu	Ser	Leu	Ser	Gly	Glu	Tyr	Val	
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Arg	Ala	Arg	Ile	Lys	Gly	Val	Asn	Tyr	Glu	Pro	Ile	Asp	Arg	Thr	Lys	
385								390		395						
Tyr	Thr	Lys	Val	Leu	Trp	Asp	Phe	Asn	Asp	Gly	Thr	Lys	Gln	Gly	Phe	
								410								
Gly	Val	Asn	Gly	Asp	Ser	Pro	Val	Glu	Asp	Val	Val	Ile	Glu	Asn	Glu	
								425								
Ala	Gly	Ala	Leu	Lys	Leu	Ser	Gly	Leu	Asp	Ala	Ser	Asn	Asp	Val	Ser	
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Lys	Ser	Val	Asp	Ile	Leu	Gly	Ala	Glu	Lys	Leu	Thr	Met	Asp	Val	Ile	
465								470		475						
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Ser	Ala	Asn	Trp	Val	Asn	Pro	Asn	Arg	Ala	Ile	Lys	Val	Glu	Pro	Thr	
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Pro	Val	Val	His	Asp	Pro	Lys	Gly	Glu	Ala	Val	Leu	Pro	Ser	Val	Phe	
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Glu	Asp	Gly	Thr	Arg	Gln	Gly	Trp	Asp	Trp	Ala	Gly	Glu	Ser	Gly	Val	
								600								
Lys	Thr	Ala	Leu	Thr	Ile	Glu	Glu	Ala	Asn	Gly	Ser	Asn	Ala	Leu	Ser	
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Trp	Glu	Phe	Gly	Tyr	Pro	Glu	Val	Lys	Pro	Ser	Asp	Asn	Trp	Ala	Thr	
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Ala	Pro	Arg	Leu	Asp	Phe	Trp	Lys	Ser	Asp	Leu	Val	Arg	Gly	Glu	Asn	
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Asp	Tyr	Val	Thr	Phe	Asp	Phe	Tyr	Leu	Asp	Pro	Val	Arg	Ala	Thr	Glu	
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Gly	Ala	Met	Asn	Ile	Asn	Leu	Val	Phe	Gln	Pro	Pro	Thr	Asn	Gly	Tyr	
675								680								

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 Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg Asn Met  
 725 730 735  
 Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg Val Phe  
 740 745 750  
 Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro Val Glu  
 755 760 765  
 Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys  
 770 775 780  
 Glu Ala Lys Thr Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys Glu Glu  
 785 790 795 800

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 <212> TYPE: DNA  
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 <220> FEATURE:  
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ctaactacat agataaagga agataaaatg aacaattata aactaatgat tcaatatgat      180
ggtggtcgat acaaaggttg gcagcgtctt gggaacggtg aaaatacgat tcaaggtaaa      240
attgaaacgg ttttatcaga gatggttagt agaaaaatag agattatagg gtctggtaga      300
acagatgctg gtgtccatgc tcttgacaa gtggctaattg taaaattaag cgaaaatttt      360
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gaggtgacgc tagttccaga tcgttttcac tcaaggata acgcaaagga caaacctat      480
ctttataaaa ttggaatga ggattatact catccgttta tgcgtaagta cagcttgac      540
atcgaaaaga aattacatat tgataacatg gtaaaagcaa gtcaactttt cgtaggagaa      600
catgatttta cagctttttc taatgctaaa tctaaaaaga agacaaatac gagaacgatt      660
cactctataa ctattcaaga taatcaagga tttatagaca ttagggtttg tggagatggt      720
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gccgatgcaa ccggcttata tttagaggga atttcttttt aaattgaata cggaataaaa      900
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Ile Ser Ser Ile Leu Ile Leu Val Leu Leu Leu Ser Leu Phe Pro Thr	
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Ala Leu Ala Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu	
30 35 40	
tta ggt aat gac aat gtt aaa cgc cct tct gag gct ggc gca tta caa	1577
Leu Gly Asn Asp Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln	
45 50 55	
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Leu Gln Glu Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu	
60 65 70	
aaa att caa tta cgt gga atg agt aca cac gga tta caa tgg ttt cct	1673
Lys Ile Gln Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro	
75 80 85	
gag atc ttg aat gat aac gca tac aaa gct ctt gct aac gat tgg gaa	1721
Glu Ile Leu Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu	
90 95 100 105	
tca aat atg att cgt cta gct atg tat gtc ggt gaa aat ggc tat gct	1769
Ser Asn Met Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala	
110 115 120	
tca aat cca gag tta att aaa agc aga gtc att aaa gga ata gat ctt	1817
Ser Asn Pro Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu	
125 130 135	
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Ala Ile Glu Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala	
140 145 150	
cct ggt gat cct aga gat ccc gtt tac gct gga gca gaa gat ttc ttt	1913
Pro Gly Asp Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe	
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Arg Asp Ile Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu	
170 175 180 185	
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Leu Ala Asn Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro	
190 195 200	
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Asn Asn Glu Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile	
205 210 215	
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Val Glu Met Leu Arg Asp Ser Gly Asn Ala Asp Asn Ile Ile Ile	
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Val Gly Ser Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn	
235 240 245	
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Pro Ile Asp Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly	
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Ser His Ala Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser	
270 275 280	
gaa aga gga aac gta atg agt aac act cgt tat gcg tta gaa aac gga	2297
Glu Arg Gly Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly	
285 290 295	
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Val Ala Val Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp	
300 305 310	

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gaa aac aac att agc tgg gct aac tgg tct tta acg aat aaa aat gaa Glu Asn Asn Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu 330 335 340 345	2441
gta tct ggt gca ttt aca cca ttc gag tta ggt aag tct aac gca aca Val Ser Gly Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr 350 355 360	2489
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ctt tct gga gaa tat gta cgt gct cgt att aaa ggt gtg aac tat gag Leu Ser Gly Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu 380 385 390	2585
cca atc gac cgt aca aaa tac acg aaa gta ctt tgg gac ttt aat gat Pro Ile Asp Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp 395 400 405	2633
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gga act gaa ggt gct gat gtt atc tat tta gat aac att aaa gta att Gly Thr Glu Gly Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile 555 560 565	3113
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gtt ctt cct tct gtt ttt gaa gac ggt aca cgt caa ggt tgg gac tgg Val Leu Pro Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp 590 595 600	3209
gct gga gag tct ggt gtg aaa aca gct tta aca att gaa gaa gca aac Ala Gly Glu Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn 605 610 615	3257
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620	625	630	
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ttg gtt cgc ggt gaa aat gat tat gta act ttt gat ttc tat cta gat Leu Val Arg Gly Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp 650 655 660 665			3401
cca gtt cgt gca aca gaa ggc gca atg aat atc aat tta gta ttc cag Pro Val Arg Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln 670 675 680			3449
cca cct act aac ggg tat tgg gta caa gca cca aaa acg tat acg att Pro Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile 685 690 695			3497
aac ttt gat gaa tta gag gaa gcg aat caa gta aat ggt tta tat cac Asn Phe Asp Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His 700 705 710			3545
tat gaa gtg aaa att aac gta aga gat att aca aac att caa gat gac Tyr Glu Val Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp 715 720 725			3593
acg tta cta cgt aac atg atg atc att ttt gca gat gta gaa agt gac Thr Leu Leu Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp 730 735 740 745			3641
ttt gca ggg aga gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct Phe Ala Gly Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala 750 755 760			3689
act act gag ccg gtt gaa cca gag cca gtt gat cct ggc gaa gag acg Thr Thr Glu Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr 765 770 775			3737
ccg cct gtc gat gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag Pro Pro Val Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu 780 785 790			3785
aaa gaa gag aaa gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa Lys Glu Glu Lys Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu 795 800 805			3833
gaa aag aaa gca atc aaa aat gag gct acg aaa aaa taatctaata Glu Lys Lys Ala Ile Lys Asn Glu Ala Thr Lys Lys 810 815 820			3879
aactagttat agggttatct aaaggctctga tgcagatctt ttagataacc tttttttgca			3939
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Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val Lys 35 40 45			
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Ser	Thr	His	Gly	Leu	Gln	Trp	Phe	Pro	Glu	Ile	Leu	Asn	Asp	Asn	Ala	85	90	95	
Tyr	Lys	Ala	Leu	Ala	Asn	Asp	Trp	Glu	Ser	Asn	Met	Ile	Arg	Leu	Ala	100	105	110	
Met	Tyr	Val	Gly	Glu	Asn	Gly	Tyr	Ala	Ser	Asn	Pro	Glu	Leu	Ile	Lys	115	120	125	
Ser	Arg	Val	Ile	Lys	Gly	Ile	Asp	Leu	Ala	Ile	Glu	Asn	Asp	Met	Tyr	130	135	140	
Val	Ile	Val	Asp	Trp	His	Val	His	Ala	Pro	Gly	Asp	Pro	Arg	Asp	Pro	145	150	155	160
Val	Tyr	Ala	Gly	Ala	Glu	Asp	Phe	Phe	Arg	Asp	Ile	Ala	Ala	Leu	Tyr	165	170	175	
Pro	Asn	Asn	Pro	His	Ile	Ile	Tyr	Glu	Leu	Ala	Asn	Glu	Pro	Ser	Ser	180	185	190	
Asn	Asn	Asn	Gly	Gly	Ala	Gly	Ile	Pro	Asn	Asn	Glu	Glu	Gly	Trp	Asn	195	200	205	
Ala	Val	Lys	Glu	Tyr	Ala	Asp	Pro	Ile	Val	Glu	Met	Leu	Arg	Asp	Ser	210	215	220	
Gly	Asn	Ala	Asp	Asp	Asn	Ile	Ile	Ile	Val	Gly	Ser	Pro	Asn	Trp	Ser	225	230	235	240
Gln	Arg	Pro	Asp	Leu	Ala	Ala	Asp	Asn	Pro	Ile	Asp	Asp	His	His	Thr	245	250	255	
Met	Tyr	Thr	Val	His	Phe	Tyr	Thr	Gly	Ser	His	Ala	Ala	Ser	Thr	Glu	260	265	270	
Ser	Tyr	Pro	Pro	Glu	Thr	Pro	Asn	Ser	Glu	Arg	Gly	Asn	Val	Met	Ser	275	280	285	
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Trp	Gly	Thr	Ser	Gln	Ala	Asn	Gly	Asp	Gly	Gly	Pro	Tyr	Phe	Asp	Glu	305	310	315	320
Ala	Asp	Val	Trp	Ile	Glu	Phe	Leu	Asn	Glu	Asn	Asn	Ile	Ser	Trp	Ala	325	330	335	
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Phe	Glu	Leu	Gly	Lys	Ser	Asn	Ala	Thr	Ser	Leu	Asp	Pro	Gly	Pro	Asp	355	360	365	
Gln	Val	Trp	Val	Pro	Glu	Glu	Leu	Ser	Leu	Ser	Gly	Glu	Tyr	Val	Arg	370	375	380	
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Thr	Lys	Val	Leu	Trp	Asp	Phe	Asn	Asp	Gly	Thr	Lys	Gln	Gly	Phe	Gly	405	410	415	
Val	Asn	Gly	Asp	Ser	Pro	Val	Glu	Asp	Val	Val	Ile	Glu	Asn	Glu	Ala	420	425	430	
Gly	Ala	Leu	Lys	Leu	Ser	Gly	Leu	Asp	Ala	Ser	Asn	Asp	Val	Ser	Glu	435	440	445	
Gly	Asn	Tyr	Trp	Ala	Asn	Ala	Arg	Leu	Ser	Ala	Asp	Gly	Trp	Gly	Lys	450	455	460	
Ser	Val	Asp	Ile	Leu	Gly	Ala	Glu	Lys	Leu	Thr	Met	Asp	Val	Ile	Val	465	470	475	480

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Phe	Val	Pro	Leu	Gly	Asp	Lys	Phe	Lys	Ala	Glu	Leu	Thr	Ile	Thr	Ser	
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Ile	Tyr	Leu	Asp	Asn	Ile	Lys	Val	Ile	Gly	Thr	Glu	Val	Glu	Ile	Pro	
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Val	Val	His	Asp	Pro	Lys	Gly	Glu	Ala	Val	Leu	Pro	Ser	Val	Phe	Glu	
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Asp	Gly	Thr	Arg	Gln	Gly	Trp	Asp	Trp	Ala	Gly	Glu	Ser	Gly	Val	Lys	
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Thr	Ala	Leu	Thr	Ile	Glu	Glu	Ala	Asn	Gly	Ser	Asn	Ala	Leu	Ser	Trp	
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Glu	Phe	Gly	Tyr	Pro	Glu	Val	Lys	Pro	Ser	Asp	Asn	Trp	Ala	Thr	Ala	
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Pro	Arg	Leu	Asp	Phe	Trp	Lys	Ser	Asp	Leu	Val	Arg	Gly	Glu	Asn	Asp	
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Tyr	Val	Thr	Phe	Asp	Phe	Tyr	Leu	Asp	Pro	Val	Arg	Ala	Thr	Glu	Gly	
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Ala	Met	Asn	Ile	Asn	Leu	Val	Phe	Gln	Pro	Pro	Thr	Asn	Gly	Tyr	Trp	
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Val	Gln	Ala	Pro	Lys	Thr	Tyr	Thr	Ile	Asn	Phe	Asp	Glu	Leu	Glu	Glu	
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Ala	Asn	Gln	Val	Asn	Gly	Leu	Tyr	His	Tyr	Glu	Val	Lys	Ile	Asn	Val	
			705			710			715					720		
Arg	Asp	Ile	Thr	Asn	Ile	Gln	Asp	Asp	Thr	Leu	Leu	Arg	Asn	Met	Met	
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Ile	Ile	Phe	Ala	Asp	Val	Glu	Ser	Asp	Phe	Ala	Gly	Arg	Val	Phe	Val	
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Glu	Pro	Val	Asp	Pro	Gly	Glu	Glu	Thr	Pro	Pro	Val	Asp	Glu	Lys	Glu	
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Ala	Lys	Lys	Glu	Gln	Lys	Glu	Ala	Glu	Lys	Glu	Glu	Lys	Glu	Ala	Val	
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Lys	Glu	Glu	Lys	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Lys	Ala	Ile	Lys	Asn	
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tgtgggtttt tattaatcaa aaaaatggta aataaaccta ttttaacaat gcttataacc	420
atTTTTctat ttattgcata aaaaaatcag taaaaaatt catttatatg tagacgtaaa	480
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tatt atg aaa ata aag caa att aaa caa tct tta tct ttg ctt tta atc	649
Met Lys Ile Lys Gln Ile Lys Gln Ser Leu Ser Leu Leu Leu Ile	
1 5 10 15	
atc aca ctc att atg tca cta ttt gtt cct atg gct tca gca aac aca	697
Ile Thr Leu Ile Met Ser Leu Phe Val Pro Met Ala Ser Ala Asn Thr	
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Asn Glu Ser Lys Ser Asn Ala Phe Pro Phe Ser Asp Val Lys Lys Thr	
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Ser Trp Ser Phe Pro Tyr Ile Lys Asp Leu Tyr Glu Gln Glu Val Ile	
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Thr Gly Thr Ser Ala Thr Thr Phe Ser Pro Thr Asp Ser Val Thr Arg	
65 70 75	
gca caa ttt aca gtg atg ctt acc cgt ggt ctt gga cta gaa gca tct	889
Ala Gln Phe Thr Val Met Leu Thr Arg Gly Leu Gly Leu Glu Ala Ser	
80 85 90 95	
tct aaa gat tac cct ttt aaa gat cgt aaa aac tgg gct tac aaa gaa	937
Ser Lys Asp Tyr Pro Phe Lys Asp Arg Lys Asn Trp Ala Tyr Lys Glu	
100 105 110	
att caa gct gca tat gaa gct gga att gta act ggg aaa aca aac ggt	985
Ile Gln Ala Ala Tyr Glu Ala Gly Ile Val Thr Gly Lys Thr Asn Gly	
115 120 125	
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Glu Phe Ala Pro Asn Glu Asn Ile Thr Arg Glu Gln Met Ala Ala Met	
130 135 140	
gcc gta cgt gct tat gaa tac tta gaa aat gag cta tct tta cca gaa	1081
Ala Val Arg Ala Tyr Glu Tyr Leu Glu Asn Glu Leu Ser Leu Pro Glu	
145 150 155	
gag caa aga gaa tat aat gac tct tct tct att tca acc ttt gct caa	1129
Glu Gln Arg Glu Tyr Asn Asp Ser Ser Ser Ile Ser Thr Phe Ala Gln	
160 165 170 175	
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Asp Ala Val Gln Lys Ala Tyr Val Leu Glu Leu Met Glu Gly Asn Thr	
180 185 190	
gat gga tat ttt caa cca aaa aga aac tct act aga gaa cag tct gct	1225
Asp Gly Tyr Phe Gln Pro Lys Arg Asn Ser Thr Arg Glu Gln Ser Ala	
195 200 205	
aaa gtt atc tct act tta ctt tgg aaa gta gct agt cat gat tat tta	1273
Lys Val Ile Ser Thr Leu Leu Trp Lys Val Ala Ser His Asp Tyr Leu	
210 215 220	
tac cat aca gaa gct gtt aaa agc cct tca gaa gct ggt gcg ctt cag	1321
Tyr His Thr Glu Ala Val Lys Ser Pro Ser Glu Ala Gly Ala Leu Gln	
225 230 235	
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Pro	Val	Gln	Leu	Arg	Gly	Met	Ser	Thr	His	Gly	Leu	Gln	Trp	Phe	Gly	
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gaa	atc	gta	aac	gaa	aac	gct	ttc	gta	gca	cta	tcg	aat	gat	tgg	gga	1465
Glu	Ile	Val	Asn	Glu	Asn	Ala	Phe	Val	Ala	Leu	Ser	Asn	Asp	Trp	Gly	
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tct	aac	atg	att	cgt	ctc	gct	atg	tac	att	ggc	gaa	aat	gga	tat	gca	1513
Ser	Asn	Met	Ile	Arg	Leu	Ala	Met	Tyr	Ile	Gly	Glu	Asn	Gly	Tyr	Ala	
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Thr	Asn	Pro	Glu	Val	Lys	Asp	Leu	Val	Tyr	Glu	Gly	Ile	Glu	Leu	Ala	
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Phe	Glu	His	Asp	Met	Tyr	Val	Ile	Val	Asp	Trp	His	Val	His	Ala	Pro	
320					325					330					335	
ggt	gat	cct	aga	gcg	gat	gta	tac	tca	ggt	gct	tat	gat	ttc	ttc	gaa	1657
Gly	Asp	Pro	Arg	Ala	Asp	Val	Tyr	Ser	Gly	Ala	Tyr	Asp	Phe	Phe	Glu	
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gaa	att	gct	gat	cat	tac	aaa	gat	cat	ccg	aaa	aac	cat	tat	atc	att	1705
Glu	Ile	Ala	Asp	His	Tyr	Lys	Asp	His	Pro	Lys	Asn	His	Tyr	Ile	Ile	
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Trp	Glu	Leu	Ala	Asn	Glu	Pro	Ser	Pro	Asn	Asn	Asn	Gly	Gly	Pro	Gly	
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Leu	Thr	Asn	Asp	Glu	Lys	Gly	Trp	Glu	Ala	Val	Lys	Glu	Tyr	Ala	Glu	
	385					390					395					
cca	atc	gtt	gaa	atg	ttg	cgt	gaa	aaa	ggt	gac	aac	atg	att	tta	gtt	1849
Pro	Ile	Val	Glu	Met	Leu	Arg	Glu	Lys	Gly	Asp	Asn	Met	Ile	Leu	Val	
400					405					410					415	
gga	aat	cct	aac	tgg	agc	caa	cgt	cct	gac	tta	tca	gct	gac	aac	cca	1897
Gly	Asn	Pro	Asn	Trp	Ser	Gln	Arg	Pro	Asp	Leu	Ser	Ala	Asp	Asn	Pro	
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att	gat	gca	gaa	aat	atc	atg	tat	tct	gtt	cac	ttc	tac	aca	ggc	tca	1945
Ile	Asp	Ala	Glu	Asn	Ile	Met	Tyr	Ser	Val	His	Phe	Tyr	Thr	Gly	Ser	
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cgt	tct	aat	gtt	atg	gct	aac	gtt	cgt	tat	gct	cta	gac	aat	ggc	gtt	2041
Arg	Ser	Asn	Val	Met	Ala	Asn	Val	Arg	Tyr	Ala	Leu	Asp	Asn	Gly	Val	
	465					470					475					
gct	gtg	ttt	gcg	aca	gag	tgg	ggt	acg	agt	caa	gcg	aat	gga	gat	gga	2089
Ala	Val	Phe	Ala	Thr	Glu	Trp	Gly	Thr	Ser	Gln	Ala	Asn	Gly	Asp	Gly	
480					485					490				495		
gga	cct	tat	ttt	gat	gaa	gct	gat	gtt	tgg	ctt	aat	ttc	tta	aac	aaa	2137
Gly	Pro	Tyr	Phe	Asp	Glu	Ala	Asp	Val	Trp	Leu	Asn	Phe	Leu	Asn	Lys	
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cat	aac	att	agc	tgg	gca	aac	tgg	tcg	tta	acg	aac	aaa	aat	gag	att	2185
His	Asn	Ile	Ser	Trp	Ala	Asn	Trp	Ser	Leu	Thr	Asn	Lys	Asn	Glu	Ile	
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Ser	Gly	Ala	Phe	Thr	Pro	Phe	Glu	Leu	Gly	Arg	Thr	Asp	Ala	Thr	Asp	
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ctt	gat	cca	ggt	gct	aat	caa	gta	tgg	gca	ccc	gag	gaa	cta	agt	tta	2281
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Ile Asp Arg Thr Lys Phe Thr Lys Leu Val Trp Asp Phe Asn Asp Gly	
580 585 590	
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Thr Thr Gln Gly Phe Gln Val Asn Gly Asp Ser Pro Asn Lys Glu Ser	
595 600 605	
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Ile Thr Leu Ser Asn Asn Asn Asp Ala Leu Gln Ile Glu Gly Leu Asn	
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Val Ser Asn Asp Ile Ser Glu Gly Asn Tyr Trp Asp Asn Val Arg Leu	
625 630 635	
tca gct gat ggc tgg agt gaa aat gta gat att tta ggt gct aca gag	2569
Ser Ala Asp Gly Trp Ser Glu Asn Val Asp Ile Leu Gly Ala Thr Glu	
640 645 650 655	
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Leu Thr Ile Asp Val Ile Val Glu Glu Pro Thr Thr Val Ser Ile Ala	
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gct att cca caa gga cct gct gct ggc tgg gct aac ccg act aga gca	2665
Ala Ile Pro Gln Gly Pro Ala Ala Gly Trp Ala Asn Pro Thr Arg Ala	
675 680 685	
att aaa gta act gaa gac gat ttc gaa tct ttc gga gat gga tac aaa	2713
Ile Lys Val Thr Glu Asp Asp Phe Glu Ser Phe Gly Asp Gly Tyr Lys	
690 695 700	
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Ala Thr Ser Pro Glu Asp Asn Thr Met Ser Asn Ile Ile Leu Phe Val	
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740 745 750	
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Gly Thr Glu Ile Glu Ile Glu Val Ile His Asp Glu Lys Gly Thr Ala	
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aca ctt cct tct act ttt gaa gat gga act cgc caa ggc tgg gat tgg	2953
Thr Leu Pro Ser Thr Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp	
770 775 780	
cat aca gaa tca gga gtt aag aca gct ctt aca att gaa gaa gct aat	3001
His Thr Glu Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn	
785 790 795	
gga tct aac gct ctt tca tgg gaa tat gcg tat cct gaa gta aaa cca	3049
Gly Ser Asn Ala Leu Ser Trp Glu Tyr Ala Tyr Pro Glu Val Lys Pro	
800 805 810 815	
agt gat ggt tgg gct act gct cct cgt cta gac ttc tgg aaa gac gaa	3097
Ser Asp Gly Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Asp Glu	
820 825 830	
cta gtt cgt ggc aca agc gac tat att agt ttt gac ttt tac atc gat	3145
Leu Val Arg Gly Thr Ser Asp Tyr Ile Ser Phe Asp Phe Tyr Ile Asp	
835 840 845	
gca gtt cgt gct tct gaa ggt gct ata tca att aac gcc gtt ttc caa	3193
Ala Val Arg Ala Ser Glu Gly Ala Ile Ser Ile Asn Ala Val Phe Gln	
850 855 860	
cca cct gca aac ggg tat tgg caa gaa gtt cca act aca ttt gaa att	3241
Pro Pro Ala Asn Gly Tyr Trp Gln Glu Val Pro Thr Thr Phe Glu Ile	
865 870 875	

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gat tta aca gag ctt gat tct gca act gta act tct gat gag ttg tat      3289
Asp Leu Thr Glu Leu Asp Ser Ala Thr Val Thr Ser Asp Glu Leu Tyr
880                      885                      890                      895

cat tat gaa gta aaa att aac att aga gac att gag gct att aca gac      3337
His Tyr Glu Val Lys Ile Asn Ile Arg Asp Ile Glu Ala Ile Thr Asp
                      900                      905                      910

gat aca gag ctt cgt aac tta tta cta atc ttt gct gat gaa gac agt      3385
Asp Thr Glu Leu Arg Asn Leu Leu Leu Ile Phe Ala Asp Glu Asp Ser
                      915                      920                      925

gat ttt gct ggt aga gtt ttt gtt gat aat gta aga ttt gaa      3427
Asp Phe Ala Gly Arg Val Phe Val Asp Asn Val Arg Phe Glu
                      930                      935                      940

taatttaaaa acagtagata gagagactct ctatctacct gtttattgct tactattcgt      3487

cttccacttt t      3498

<210> SEQ ID NO 10
<211> LENGTH: 941
<212> TYPE: PRT
<213> ORGANISM: Bacillus sp. KSM-635

<400> SEQUENCE: 10

Met Lys Ile Lys Gln Ile Lys Gln Ser Leu Ser Leu Leu Leu Ile Ile
1                      5                      10                      15

Thr Leu Ile Met Ser Leu Phe Val Pro Met Ala Ser Ala Asn Thr Asn
20                      25                      30

Glu Ser Lys Ser Asn Ala Phe Pro Phe Ser Asp Val Lys Lys Thr Ser
35                      40                      45

Trp Ser Phe Pro Tyr Ile Lys Asp Leu Tyr Glu Gln Glu Val Ile Thr
50                      55                      60

Gly Thr Ser Ala Thr Thr Phe Ser Pro Thr Asp Ser Val Thr Arg Ala
65                      70                      75                      80

Gln Phe Thr Val Met Leu Thr Arg Gly Leu Gly Leu Glu Ala Ser Ser
85                      90                      95

Lys Asp Tyr Pro Phe Lys Asp Arg Lys Asn Trp Ala Tyr Lys Glu Ile
100                     105                     110

Gln Ala Ala Tyr Glu Ala Gly Ile Val Thr Gly Lys Thr Asn Gly Glu
115                     120                     125

Phe Ala Pro Asn Glu Asn Ile Thr Arg Glu Gln Met Ala Ala Met Ala
130                     135                     140

Val Arg Ala Tyr Glu Tyr Leu Glu Asn Glu Leu Ser Leu Pro Glu Glu
145                     150                     155                     160

Gln Arg Glu Tyr Asn Asp Ser Ser Ser Ile Ser Thr Phe Ala Gln Asp
165                     170                     175

Ala Val Gln Lys Ala Tyr Val Leu Glu Leu Met Glu Gly Asn Thr Asp
180                     185                     190

Gly Tyr Phe Gln Pro Lys Arg Asn Ser Thr Arg Glu Gln Ser Ala Lys
195                     200                     205

Val Ile Ser Thr Leu Leu Trp Lys Val Ala Ser His Asp Tyr Leu Tyr
210                     215                     220

His Thr Glu Ala Val Lys Ser Pro Ser Glu Ala Gly Ala Leu Gln Leu
225                     230                     235                     240

Val Glu Leu Asn Gly Gln Leu Thr Leu Ala Gly Glu Asp Gly Thr Pro
245                     250                     255

Val Gln Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Gly Glu
260                     265                     270

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Ile Val Asn Glu Asn Ala Phe Val Ala Leu Ser Asn Asp Trp Gly Ser	275	280	285
Asn Met Ile Arg Leu Ala Met Tyr Ile Gly Glu Asn Gly Tyr Ala Thr	290	295	300
Asn Pro Glu Val Lys Asp Leu Val Tyr Glu Gly Ile Glu Leu Ala Phe	305	310	315 320
Glu His Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly	325	330	335
Asp Pro Arg Ala Asp Val Tyr Ser Gly Ala Tyr Asp Phe Phe Glu Glu	340	345	350
Ile Ala Asp His Tyr Lys Asp His Pro Lys Asn His Tyr Ile Ile Trp	355	360	365
Glu Leu Ala Asn Glu Pro Ser Pro Asn Asn Asn Gly Gly Pro Gly Leu	370	375	380
Thr Asn Asp Glu Lys Gly Trp Glu Ala Val Lys Glu Tyr Ala Glu Pro	385	390	395 400
Ile Val Glu Met Leu Arg Glu Lys Gly Asp Asn Met Ile Leu Val Gly	405	410	415
Asn Pro Asn Trp Ser Gln Arg Pro Asp Leu Ser Ala Asp Asn Pro Ile	420	425	430
Asp Ala Glu Asn Ile Met Tyr Ser Val His Phe Tyr Thr Gly Ser His	435	440	445
Gly Ala Ser His Ile Gly Tyr Pro Glu Gly Thr Pro Ser Ser Glu Arg	450	455	460
Ser Asn Val Met Ala Asn Val Arg Tyr Ala Leu Asp Asn Gly Val Ala	465	470	475 480
Val Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly	485	490	495
Pro Tyr Phe Asp Glu Ala Asp Val Trp Leu Asn Phe Leu Asn Lys His	500	505	510
Asn Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Ile Ser	515	520	525
Gly Ala Phe Thr Pro Phe Glu Leu Gly Arg Thr Asp Ala Thr Asp Leu	530	535	540
Asp Pro Gly Ala Asn Gln Val Trp Ala Pro Glu Glu Leu Ser Leu Ser	545	550	555 560
Gly Glu Tyr Val Arg Ala Arg Ile Lys Gly Ile Glu Tyr Thr Pro Ile	565	570	575
Asp Arg Thr Lys Phe Thr Lys Leu Val Trp Asp Phe Asn Asp Gly Thr	580	585	590
Thr Gln Gly Phe Gln Val Asn Gly Asp Ser Pro Asn Lys Glu Ser Ile	595	600	605
Thr Leu Ser Asn Asn Asn Asp Ala Leu Gln Ile Glu Gly Leu Asn Val	610	615	620
Ser Asn Asp Ile Ser Glu Gly Asn Tyr Trp Asp Asn Val Arg Leu Ser	625	630	635 640
Ala Asp Gly Trp Ser Glu Asn Val Asp Ile Leu Gly Ala Thr Glu Leu	645	650	655
Thr Ile Asp Val Ile Val Glu Glu Pro Thr Thr Val Ser Ile Ala Ala	660	665	670
Ile Pro Gln Gly Pro Ala Ala Gly Trp Ala Asn Pro Thr Arg Ala Ile	675	680	685

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Lys Val Thr Glu Asp Asp Phe Glu Ser Phe Gly Asp Gly Tyr Lys Ala  
 690 695 700  
 Leu Val Thr Ile Thr Ser Glu Asp Ser Pro Ser Leu Glu Thr Ile Ala  
 705 710 715 720  
 Thr Ser Pro Glu Asp Asn Thr Met Ser Asn Ile Ile Leu Phe Val Gly  
 725 730 735  
 Thr Glu Asp Ala Asp Val Ile Ser Leu Asp Asn Ile Thr Val Ser Gly  
 740 745 750  
 Thr Glu Ile Glu Ile Glu Val Ile His Asp Glu Lys Gly Thr Ala Thr  
 755 760 765  
 Leu Pro Ser Thr Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp His  
 770 775 780  
 Thr Glu Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly  
 785 790 795 800  
 Ser Asn Ala Leu Ser Trp Glu Tyr Ala Tyr Pro Glu Val Lys Pro Ser  
 805 810 815  
 Asp Gly Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Asp Glu Leu  
 820 825 830  
 Val Arg Gly Thr Ser Asp Tyr Ile Ser Phe Asp Phe Tyr Ile Asp Ala  
 835 840 845  
 Val Arg Ala Ser Glu Gly Ala Ile Ser Ile Asn Ala Val Phe Gln Pro  
 850 855 860  
 Pro Ala Asn Gly Tyr Trp Gln Glu Val Pro Thr Thr Phe Glu Ile Asp  
 865 870 875 880  
 Leu Thr Glu Leu Asp Ser Ala Thr Val Thr Ser Asp Glu Leu Tyr His  
 885 890 895  
 Tyr Glu Val Lys Ile Asn Ile Arg Asp Ile Glu Ala Ile Thr Asp Asp  
 900 905 910  
 Thr Glu Leu Arg Asn Leu Leu Leu Ile Phe Ala Asp Glu Asp Ser Asp  
 915 920 925  
 Phe Ala Gly Arg Val Phe Val Asp Asn Val Arg Phe Glu  
 930 935 940

<210> SEQ ID NO 11  
 <211> LENGTH: 2708  
 <212> TYPE: DNA  
 <213> ORGANISM: Bacillus sp. N-4  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (231)..(2705)

<400> SEQUENCE: 11

tttcttacaa aaaaggggtg ttctataaat agtagatgac tagactttct agttcagctt	60
actatttttg gaatagcgaa atttttataa tgggtttacga aaccactttc gtatttaggt	120
tacattatgtt tgattgtacg aaagttacat attttatttc gttttaaata ttccgaaacg	180
taaaggtgga ctccgataag tgacaaacga cattaatggg aggggttcata gtg agg	236
Val Arg	
1	
aac aaa tta aga cgt tta tta gca att atg atg gct gtt ctt tta att	284
Asn Lys Leu Arg Arg Leu Leu Ala Ile Met Met Ala Val Leu Leu Ile	
5 10 15	
act tca ttg ttt gca cca atg gtg agt gca gaa gaa ggt gat aat gga	332
Thr Ser Leu Phe Ala Pro Met Val Ser Ala Glu Glu Gly Asp Asn Gly	
20 25 30	
gat gac gat gat tta gta act cca att gaa att gaa gaa aga cct cat	380
Asp Asp Asp Asp Leu Val Thr Pro Ile Glu Ile Glu Glu Arg Pro His	

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35	40	45	50	
gag tca aat tat gag aaa tat ccg gcg cta tta gat gga gga cta gat Glu Ser Asn Tyr Glu Lys Tyr Pro Ala Leu Leu Asp Gly Gly Leu Asp 55 60 65				428
gaa aga aga cct tca gaa gct ggt gca tta caa ttg gtt gaa gta gat Glu Arg Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Val Glu Val Asp 70 75 80				476
gga caa gtt act tta gca gat caa gat ggt gtt cca att caa tta cgt Gly Gln Val Thr Leu Ala Asp Gln Asp Gly Val Pro Ile Gln Leu Arg 85 90 95				524
ggg atg agt aca cac ggt tta caa tgg ttt ggc gaa atc gta aat gaa Gly Met Ser Thr His Gly Leu Gln Trp Phe Gly Glu Ile Val Asn Glu 100 105 110				572
aac gct ttt gca gcg tta gca aat gat tgg gga tct aat gta att aga Asn Ala Phe Ala Ala Leu Ala Asn Asp Trp Gly Ser Asn Val Ile Arg 115 120 125 130				620
tta gcg cta tat atc gga gaa aat gcg tat cgt tac aac cca gat ctt Leu Ala Leu Tyr Ile Gly Glu Asn Ala Tyr Arg Tyr Asn Pro Asp Leu 135 140 145				668
att gaa aag gta tat gca ggg ata gaa tta gcg aaa gaa aac gat atg Ile Glu Lys Val Tyr Ala Gly Ile Glu Leu Ala Lys Glu Asn Asp Met 150 155 160				716
tat gtc att att gat tgg cat gtt cat gca cct ggt gac cct aat gct Tyr Val Ile Ile Asp Trp His Val His Ala Pro Gly Asp Pro Asn Ala 165 170 175				764
gac att tac caa ggt ggc gtt aat gaa gat gga gaa gaa tat tta gga Asp Ile Tyr Gln Gly Gly Val Asn Glu Asp Gly Glu Glu Tyr Leu Gly 180 185 190				812
gct aaa gat ttc ttc tta cac att gct gaa aag tac cca aat gac cca Ala Lys Asp Phe Phe Leu His Ile Ala Glu Lys Tyr Pro Asn Asp Pro 195 200 205 210				860
cat cta att tat gag ctt gca aac gag cca agc tca aat agt agc ggt His Leu Ile Tyr Glu Leu Ala Asn Glu Pro Ser Ser Asn Ser Ser Gly 215 220 225				908
ggc cct ggg ata acg aat gat gag gac gga tgg gaa gca gtt aga gaa Gly Pro Gly Ile Thr Asn Asp Glu Asp Gly Trp Glu Ala Val Arg Glu 230 235 240				956
tat gct caa cct atc gta gat gca ctt cgt gat agt gga aat gct gaa Tyr Ala Gln Pro Ile Val Asp Ala Leu Arg Asp Ser Gly Asn Ala Glu 245 250 255				1004
gat aac att att atc gta ggt agc cct aac tgg agt caa aga atg gat Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp Ser Gln Arg Met Asp 260 265 270				1052
tta gct gct gct gat aat cca att gat gac cat cat aca atg tat aca Leu Ala Ala Ala Asp Asn Pro Ile Asp Asp His His Thr Met Tyr Thr 275 280 285 290				1100
cta cat ttc tat act ggt act cac gaa gga aca aat gag agt tat cca Leu His Phe Tyr Thr Gly Thr His Glu Gly Thr Asn Glu Ser Tyr Pro 295 300 305				1148
gaa ggt ata tct agc gag gat cgc agt aac gta atg gct aac gca aaa Glu Gly Ile Ser Ser Glu Asp Arg Ser Asn Val Met Ala Asn Ala Lys 310 315 320				1196
tac gca cta gat aaa gga aaa gca atc ttt gca aca gag tgg ggc gta Tyr Ala Leu Asp Lys Gly Lys Ala Ile Phe Ala Thr Glu Trp Gly Val 325 330 335				1244
agt gaa gct gac ggt aat aat ggt cct tac tta aat gaa gca gat gtc Ser Glu Ala Asp Gly Asn Asn Gly Pro Tyr Leu Asn Glu Ala Asp Val 340 345 350				1292
tgg ctt aat ttt cta aat gaa aac aac att agc tgg act aac tgg tct				1340

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Trp	Leu	Asn	Phe	Leu	Asn	Glu	Asn	Asn	Ile	Ser	Trp	Thr	Asn	Trp	Ser	
355					360					365					370	
tta	aca	aat	aaa	aat	gaa	act	tct	ggt	gca	ttt	aca	cca	ttt	att	tta	1388
Leu	Thr	Asn	Lys	Asn	Glu	Thr	Ser	Gly	Ala	Phe	Thr	Pro	Phe	Ile	Leu	
			375						380					385		
aat	gaa	tct	gat	gca	act	gat	ctt	gac	cca	ggt	gaa	gat	caa	gta	tgg	1436
Asn	Glu	Ser	Asp	Ala	Thr	Asp	Leu	Asp	Pro	Gly	Glu	Asp	Gln	Val	Trp	
			390					395					400			
tct	atg	gaa	gaa	tta	agt	gta	tct	ggt	gaa	tac	gta	cgt	tca	cgt	ata	1484
Ser	Met		Glu	Glu	Leu	Ser	Val	Ser	Gly	Glu	Tyr	Val	Arg	Ser	Arg	
		405					410					415				
ttg	gga	gaa	gaa	tat	cag	cca	att	gat	cgt	aca	cca	aga	gag	gaa	ttc	1532
Leu	Gly	Glu	Glu	Tyr	Gln	Pro	Ile	Asp	Arg	Thr	Pro	Arg	Glu	Glu	Phe	
	420					425					430					
tct	gaa	gta	att	tgg	gac	ttt	aac	gac	ggg	act	aca	caa	ggg	ttt	gta	1580
Ser	Glu	Val	Ile	Trp	Asp	Phe	Asn	Asp	Gly	Thr	Thr	Gln	Gly	Phe	Val	
435					440				445						450	
caa	aat	agt	gat	agc	cct	cta	gat	gta	act	att	gaa	aat	gta	aat	gac	1628
Gln	Asn	Ser	Asp	Ser	Pro	Leu	Asp	Val	Thr	Ile	Glu	Asn	Val	Asn	Asp	
			455						460					465		
gca	ctt	caa	atc	acc	ggt	tta	gat	gaa	agt	aac	gct	att	gct	gga	gaa	1676
Ala	Leu	Gln	Ile	Thr	Gly	Leu	Asp	Glu	Ser	Asn	Ala	Ile	Ala	Gly	Glu	
		470						475					480			
gaa	gaa	gat	tac	tgg	tcg	aat	gta	cga	att	tct	gca	gat	gaa	tgg	gaa	1724
Glu	Glu	Asp	Tyr	Trp	Ser	Asn	Val	Arg	Ile	Ser	Ala	Asp	Glu	Trp	Glu	
		485				490						495				
gaa	aca	ttt	gac	ata	cta	ggt	gca	gag	gag	tta	tcg	atg	gac	gtt	gta	1772
Glu	Thr	Phe	Asp	Ile	Leu	Gly	Ala	Glu	Glu	Leu	Ser	Met	Asp	Val	Val	
	500					505					510					
gtt	gat	gat	cca	act	aca	gta	gcc	att	gca	gca	att	cct	caa	agt	agt	1820
Val	Asp	Asp	Pro	Thr	Thr	Val	Ala	Ile	Ala	Ala	Ile	Pro	Gln	Ser	Ser	
	515				520				525						530	
gct	cat	gaa	tgg	gcg	aac	gca	tct	aat	tcc	gtt	tta	ata	acg	gaa	gat	1868
Ala	His	Glu	Trp	Ala	Asn	Ala	Ser	Asn	Ser	Val	Leu	Ile	Thr	Glu	Asp	
			535						540						545	
gac	ttt	gaa	gaa	caa	gaa	gat	ggc	aca	tac	aaa	gca	ctc	tta	acc	atc	1916
Asp	Phe	Glu	Glu	Gln	Glu	Asp	Gly	Thr	Tyr	Lys	Ala	Leu	Leu	Thr	Ile	
		550					555					560				
acg	ggt	gaa	gat	gca	cca	aat	ctt	aca	aac	ata	gca	gaa	gac	ccg	gaa	1964
Thr	Gly	Glu	Asp	Ala	Pro	Asn	Leu	Thr	Asn	Ile	Ala	Glu	Asp	Pro	Glu	
		565					570					575				
ggt	agt	gag	ctt	aat	aac	att	att	ctt	ttt	gtg	ggc	aca	gaa	aat	gct	2012
Gly	Ser	Glu	Leu	Asn	Asn	Ile	Ile	Leu	Phe	Val	Gly	Thr	Glu	Asn	Ala	
	580					585					590					
gat	gtg	att	tca	tta	gat	aat	att	act	gtt	aca	gga	gac	cgt	gaa	tca	2060
Asp	Val	Ile	Ser	Leu	Asp	Asn	Ile	Thr	Val	Thr	Gly	Asp	Arg	Glu	Ser	
	595				600					605				610		
gta	cca	gaa	cca	gtg	gaa	cat	gac	act	aaa	gga	gat	tca	gca	ctt	ccg	2108
Val	Pro	Glu	Pro	Val	Glu	His	Asp	Thr	Lys	Gly	Asp	Ser	Ala	Leu	Pro	
			615						620					625		
tct	gat	ttt	gaa	gat	ggt	act	cgt	caa	ggc	tgg	gag	tgg	gat	agt	gaa	2156
Ser	Asp	Phe	Glu	Asp	Gly	Thr	Arg	Gln	Gly	Trp	Glu	Trp	Asp	Ser	Glu	
		630						635					640			
tct	gca	gtt	aga	aca	gca	tta	aca	att	gaa	gag	gct	aac	gga	tca	aat	2204
Ser	Ala	Val	Arg	Thr	Ala	Leu	Thr	Ile	Glu	Glu	Ala	Asn	Gly	Ser	Asn	
		645					650					655				
gct	ctt	tca	tgg	gaa	tat	gca	tac	cca	gaa	gtg	aag	cca	agt	gat	gat	2252
Ala	Leu	Ser	Trp	Glu	Tyr	Ala	Tyr	Pro	Glu	Val	Lys	Pro	Ser	Asp	Asp	
	660					665					670					



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tgg gct act gcg cca aga cta aca tta tat aaa gat gat tta gtt cgt	2300
Trp Ala Thr Ala Pro Arg Leu Thr Leu Tyr Lys Asp Asp Leu Val Arg	
675 680 685 690	
ggc gat tat gaa ttt gta gcc ttt gat ttt tac att gat cca att gaa	2348
Gly Asp Tyr Glu Phe Val Ala Phe Asp Phe Tyr Ile Asp Pro Ile Glu	
695 700 705	
gat aga gct aca gaa ggt gct att gat att aac tta att ttt caa cgg	2396
Asp Arg Ala Thr Glu Gly Ala Ile Asp Ile Asn Leu Ile Phe Gln Pro	
710 715 720	
cca gcg gca gga tat tgg gct caa gca tct gaa aca ttt gaa att gat	2444
Pro Ala Ala Gly Tyr Trp Ala Gln Ala Ser Glu Thr Phe Glu Ile Asp	
725 730 735	
cta gaa gaa cta gat tct gct acg gta aca gac gat ggc cta tat cat	2492
Leu Glu Glu Leu Asp Ser Ala Thr Val Thr Asp Asp Gly Leu Tyr His	
740 745 750	
tat gag gta gag att aat att gaa gat atc gaa aat gat att gag tta	2540
Tyr Glu Val Glu Ile Asn Ile Glu Asp Ile Glu Asn Asp Ile Glu Leu	
755 760 765 770	
cgt aat cta atg ctt att ttc gca gac gat gaa agt gac ttt gct gga	2588
Arg Asn Leu Met Leu Ile Phe Ala Asp Asp Glu Ser Asp Phe Ala Gly	
775 780 785	
aga gta ttt ctt gat aat gta aga atg gat atg tct tta gaa aca aaa	2636
Arg Val Phe Leu Asp Asn Val Arg Met Asp Met Ser Leu Glu Thr Lys	
790 795 800	
gta gaa gta cta gaa aga aat ata aat gaa ttg caa gaa cag tta gta	2684
Val Glu Val Leu Glu Arg Asn Ile Asn Glu Leu Gln Glu Gln Leu Val	
805 810 815	
gaa gta gaa gct tta atg cgg tag	2708
Glu Val Glu Ala Leu Met Arg	
820 825	

&lt;210&gt; SEQ ID NO 12

&lt;211&gt; LENGTH: 825

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Bacillus sp. N-4

&lt;400&gt; SEQUENCE: 12

Val Arg Asn Lys Leu Arg Arg Leu Leu Ala Ile Met Met Ala Val Leu	
1 5 10 15	
Leu Ile Thr Ser Leu Phe Ala Pro Met Val Ser Ala Glu Glu Gly Asp	
20 25 30	
Asn Gly Asp Asp Asp Asp Leu Val Thr Pro Ile Glu Ile Glu Glu Arg	
35 40 45	
Pro His Glu Ser Asn Tyr Glu Lys Tyr Pro Ala Leu Leu Asp Gly Gly	
50 55 60	
Leu Asp Glu Arg Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Val Glu	
65 70 75 80	
Val Asp Gly Gln Val Thr Leu Ala Asp Gln Asp Gly Val Pro Ile Gln	
85 90 95	
Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Gly Glu Ile Val	
100 105 110	
Asn Glu Asn Ala Phe Ala Ala Leu Ala Asn Asp Trp Gly Ser Asn Val	
115 120 125	
Ile Arg Leu Ala Leu Tyr Ile Gly Glu Asn Ala Tyr Arg Tyr Asn Pro	
130 135 140	
Asp Leu Ile Glu Lys Val Tyr Ala Gly Ile Glu Leu Ala Lys Glu Asn	
145 150 155 160	
Asp Met Tyr Val Ile Ile Asp Trp His Val His Ala Pro Gly Asp Pro	

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165								170					175				
Asn	Ala	Asp	Ile 180	Tyr	Gln	Gly	Gly	Val 185	Asn	Glu	Asp	Gly	Glu 190	Glu	Tyr		
Leu	Gly	Ala	Lys 195	Asp	Phe	Phe	Leu 200	His	Ile	Ala	Glu	Lys 205	Tyr	Pro	Asn		
Asp	Pro	His	Leu 210	Ile	Tyr	Glu 215	Leu	Ala	Asn	Glu	Pro 220	Ser	Ser	Asn	Ser		
Ser 225	Gly	Gly	Pro	Gly	Ile 230	Thr	Asn	Asp	Glu	Asp 235	Gly	Trp	Glu	Ala	Val 240		
Arg	Glu	Tyr	Ala 245	Gln	Pro	Ile	Val	Asp 250	Ala	Leu	Arg	Asp	Ser	Gly 255	Asn		
Ala	Glu	Asp	Asn 260	Ile	Ile	Ile	Val	Gly 265	Ser	Pro	Asn	Trp	Ser 270	Gln	Arg		
Met	Asp	Leu 275	Ala	Ala	Ala	Asp	Asn 280	Pro	Ile	Asp	Asp	His 285	His	Thr	Met		
Tyr	Thr 290	Leu	His	Phe	Tyr	Thr 295	Gly	Thr	His	Glu	Gly 300	Thr	Asn	Glu	Ser		
Tyr 305	Pro	Glu	Gly	Ile	Ser 310	Ser	Glu	Asp	Arg	Ser 315	Asn	Val	Met	Ala	Asn 320		
Ala	Lys	Tyr	Ala 325	Leu	Asp	Lys	Gly	Lys	Ala 330	Ile	Phe	Ala	Thr	Glu 335	Trp		
Gly	Val	Ser	Glu 340	Ala	Asp	Gly	Asn	Asn 345	Gly	Pro	Tyr	Leu	Asn 350	Glu	Ala		
Asp	Val	Trp 355	Leu	Asn	Phe	Leu	Asn 360	Glu	Asn	Asn	Ile	Ser 365	Trp	Thr	Asn		
Trp	Ser 370	Leu	Thr	Asn	Lys 375	Asn	Glu	Thr	Ser	Gly	Ala 380	Phe	Thr	Pro	Phe		
Ile 385	Leu	Asn	Glu	Ser	Asp 390	Ala	Thr	Asp	Leu	Asp 395	Pro	Gly	Glu	Asp	Gln 400		
Val	Trp	Ser	Met 405	Glu	Glu	Leu	Ser	Val	Ser 410	Gly	Glu	Tyr	Val	Arg 415	Ser		
Arg	Ile	Leu	Gly 420	Glu	Glu	Tyr	Gln	Pro 425	Ile	Asp	Arg	Thr	Pro 430	Arg	Glu		
Glu	Phe	Ser	Glu 435	Val	Ile	Trp	Asp 440	Phe	Asn	Asp	Gly	Thr 445	Thr	Gln	Gly		
Phe 450	Val	Gln	Asn	Ser	Asp 455	Ser	Pro	Leu	Asp	Val	Thr 460	Ile	Glu	Asn	Val		
Asn 465	Asp	Ala	Leu	Gln	Ile 470	Thr	Gly	Leu	Asp	Glu 475	Ser	Asn	Ala	Ile	Ala		
Gly	Glu	Glu	Glu 485	Asp	Tyr	Trp	Ser	Asn	Val 490	Arg	Ile	Ser	Ala	Asp 495	Glu		
Trp	Glu	Glu	Thr 500	Phe	Asp	Ile	Leu	Gly 505	Ala	Glu	Glu	Leu	Ser 510	Met	Asp		
Val	Val 515	Val	Asp	Asp	Pro	Thr	Thr 520	Val	Ala	Ile	Ala	Ala 525	Ile	Pro	Gln		
Ser 530	Ser	Ala	His	Glu	Trp 535	Ala	Asn	Ala	Ser	Asn	Ser 540	Val	Leu	Ile	Thr		
Glu 545	Asp	Asp	Phe	Glu	Glu 550	Gln	Glu	Asp	Gly	Thr 555	Tyr	Lys	Ala	Leu	Leu 560		
Thr	Ile	Thr	Gly 565	Glu	Asp	Ala	Pro	Asn	Leu 570	Thr	Asn	Ile	Ala	Glu 575	Asp		
Pro	Glu	Gly	Ser 580	Glu	Leu	Asn	Asn	Ile 585	Ile	Leu	Phe	Val 590	Gly	Thr	Glu		

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Asn Ala Asp Val Ile Ser Leu Asp Asn Ile Thr Val Thr Gly Asp Arg  
 595 600 605  
 Glu Ser Val Pro Glu Pro Val Glu His Asp Thr Lys Gly Asp Ser Ala  
 610 615 620  
 Leu Pro Ser Asp Phe Glu Asp Gly Thr Arg Gln Gly Trp Glu Trp Asp  
 625 630 635 640  
 Ser Glu Ser Ala Val Arg Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly  
 645 650 655  
 Ser Asn Ala Leu Ser Trp Glu Tyr Ala Tyr Pro Glu Val Lys Pro Ser  
 660 665 670  
 Asp Asp Trp Ala Thr Ala Pro Arg Leu Thr Leu Tyr Lys Asp Asp Leu  
 675 680 685  
 Val Arg Gly Asp Tyr Glu Phe Val Ala Phe Asp Phe Tyr Ile Asp Pro  
 690 695 700  
 Ile Glu Asp Arg Ala Thr Glu Gly Ala Ile Asp Ile Asn Leu Ile Phe  
 705 710 715 720  
 Gln Pro Pro Ala Ala Gly Tyr Trp Ala Gln Ala Ser Glu Thr Phe Glu  
 725 730 735  
 Ile Asp Leu Glu Glu Leu Asp Ser Ala Thr Val Thr Asp Asp Gly Leu  
 740 745 750  
 Tyr His Tyr Glu Val Glu Ile Asn Ile Glu Asp Ile Glu Asn Asp Ile  
 755 760 765  
 Glu Leu Arg Asn Leu Met Leu Ile Phe Ala Asp Asp Glu Ser Asp Phe  
 770 775 780  
 Ala Gly Arg Val Phe Leu Asp Asn Val Arg Met Asp Met Ser Leu Glu  
 785 790 795 800  
 Thr Lys Val Glu Val Leu Glu Arg Asn Ile Asn Glu Leu Gln Glu Gln  
 805 810 815  
 Leu Val Glu Val Glu Ala Leu Met Arg  
 820 825

<210> SEQ ID NO 13  
 <211> LENGTH: 37  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Oligonucleotide as primer (237UB1) designed  
 from the nucleotide sequence of 5'-flanking region of Bacillus sp.  
 strain KSM-S237 cellulase gene

<400> SEQUENCE: 13

ttgcggatcc aacaggctta tatttagagg aaatttc

37

<210> SEQ ID NO 14  
 <211> LENGTH: 20  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Oligonucleotide as primer (S237RV) designed  
 from the nucleotide sequence of 3'-flanking region of Bacillus sp.  
 strain KSM-S237 cellulase gene

<400> SEQUENCE: 14

tcgctaccct tttattatcg

20

<210> SEQ ID NO 15  
 <211> LENGTH: 30  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial

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<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer (Q71E-RV)
        designed from the nucleotide sequence of Bacillus sp. strain KSM-
        S237 cellulase gene

<400> SEQUENCE: 15

atTTTTtctc catgttcac tactaatgtc                               30

<210> SEQ ID NO 16
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer (Q71E-FW)
        designed from the nucleotide sequence of Bacillus sp. strain KSM-
        S237 cellulase gene

<400> SEQUENCE: 16

gacattagta gatgaacatg gagaaaaaat                               30

<210> SEQ ID NO 17
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer
        (S193R-RV) designed from the nucleotide sequence of Bacillus sp.
        strain KSM-S237 cellulase gene

<400> SEQUENCE: 17

tccaccatta ttattacgac tcggtcca                               28

<210> SEQ ID NO 18
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer
        (S193R-FW) designed from the nucleotide sequence of Bacillus sp.
        strain KSM-S237 cellulase gene

<400> SEQUENCE: 18

tgagccgagt cgtaataata atggtgga                               28

<210> SEQ ID NO 19
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer
        (Q242S-RV) designed from the nucleotide sequence of Bacillus sp.
        strain KSM-S237 cellulase gene

<400> SEQUENCE: 19

agtcggagc cgaactccag ttg                                     24

<210> SEQ ID NO 20
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer
        (Q242S-FW) designed from the nucleotide sequence of Bacillus sp.
        strain KSM-S237 cellulase gene

<400> SEQUENCE: 20

caaaactggag ttcgcgtccg gact                                   24

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<210> SEQ ID NO 21  
<211> LENGTH: 30  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer  
(N419A-RV) designed from the nucleotide sequence of Bacillus sp.  
strain KSM-S237 cellulase gene

<400> SEQUENCE: 21

tttgagaat ccgaagccac tccaaatcct 30

<210> SEQ ID NO 22  
<211> LENGTH: 30  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer  
(N419A-FW) designed from the nucleotide sequence of Bacillus sp.  
strain KSM-S237 cellulase gene

<400> SEQUENCE: 22

aggatttgga gtggcttcgg attctccaaa 30

<210> SEQ ID NO 23  
<211> LENGTH: 29  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer  
(D421A-RV) designed from the nucleotide sequence of Bacillus sp.  
strain KSM-S237 cellulase gene

<400> SEQUENCE: 23

ctttatttgg agaagccgaa ttcactcca 29

<210> SEQ ID NO 24  
<211> LENGTH: 29  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer  
(D421A-FW) designed from the nucleotide sequence of Bacillus sp.  
strain KSM-S237 cellulase gene

<400> SEQUENCE: 24

tggagtgaat tcggcttctc caaataaag 29

<210> SEQ ID NO 25  
<211> LENGTH: 30  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer  
(W454Y-RV) designed from the nucleotide sequence of Bacillus sp.  
strain KSM-S237 cellulase gene

<400> SEQUENCE: 25

agacgagcat tagcatagaa gttgccatct 30

<210> SEQ ID NO 26  
<211> LENGTH: 30  
<212> TYPE: DNA  
<213> ORGANISM: Artificial  
<220> FEATURE:  
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer  
(W454Y-FW) designed from the nucleotide sequence of Bacillus sp.  
strain KSM-S237 cellulase gene

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&lt;400&gt; SEQUENCE: 26

agatggcaac ttctatgcta atgctcgtct

30

&lt;210&gt; SEQ ID NO 27

&lt;211&gt; LENGTH: 26

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer  
(W501Y-RV) designed from the nucleotide sequence of Bacillus sp.  
strain KSM-S237 cellulase gene

&lt;400&gt; SEQUENCE: 27

ctctggattt gcatatccac ttttac

26

&lt;210&gt; SEQ ID NO 28

&lt;211&gt; LENGTH: 26

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer  
(W501Y-FW) designed from the nucleotide sequence of Bacillus sp.  
strain KSM-S237 cellulase gene

&lt;400&gt; SEQUENCE: 28

gtaaaagtgg atatgcaa at ccagag

26

&lt;210&gt; SEQ ID NO 29

&lt;211&gt; LENGTH: 28

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer  
(Q58R-RV) designed from the nucleotide sequence of Bacillus sp.  
strain KSM-S237 cellulase gene

&lt;400&gt; SEQUENCE: 29

atcgacttct tgtaattcta atgcgcca

28

&lt;210&gt; SEQ ID NO 30

&lt;211&gt; LENGTH: 28

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer  
(Q58R-FW) designed from the nucleotide sequence of Bacillus sp.  
strain KSM-S237 cellulase gene

&lt;400&gt; SEQUENCE: 30

tggcgcatta gaattacaag aagtcgat

28

&lt;210&gt; SEQ ID NO 31

&lt;211&gt; LENGTH: 28

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial

&lt;220&gt; FEATURE:

<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer  
(Q58E-RV) designed from the nucleotide sequence of Bacillus sp.  
strain KSM-S237 cellulase gene

&lt;400&gt; SEQUENCE: 31

atcgacttct tgtaaacgta atgcgcca

28

&lt;210&gt; SEQ ID NO 32

&lt;211&gt; LENGTH: 28

&lt;212&gt; TYPE: DNA

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<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer
      (Q58E-FW) designed from the nucleotide sequence of Bacillus sp.
      strain KSM-S237 cellulase gene

<400> SEQUENCE: 32

tggcgcatta cgtttacaag aagtcgat                               28

<210> SEQ ID NO 33
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer
      (A56D-FW) designed from the nucleotide sequence of Bacillus sp.
      strain KSM-S237 cellulase gene

<400> SEQUENCE: 33

tctgaggctg gcgatttaca attacaag                               28

<210> SEQ ID NO 34
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide as mutagenesis primer
      (A56D-RV) designed from the nucleotide sequence of Bacillus sp.
      strain KSM-S237 cellulase gene

<400> SEQUENCE: 34

cttgtaatg taaatcgcca gcctcaga                               28

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What is claimed is:

1. A method for enhancing anti-redeposition ability of an alkaline cellulase, or method for both enhancing anti-redeposition ability and protease resistance of an alkaline cellulase, the method comprising substituting a glutamine residue at the position corresponding to position 58 of the amino acid sequence of an alkaline cellulase as set forth in SEQ ID NO: 2 or of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, with a glutamic acid or arginine residue.

2. The method of claim 1, wherein the glutamine residue is substituted with a glutamic acid residue.

3. The method of claim 1, wherein the glutamine residue is substituted with an arginine residue.

4. The method of claim 1, wherein the alkaline cellulase that has at least 90% identity with the amino acid sequence set forth in SEQ ID NO: 2 lacks the signal sequence that corresponds to amino acids 1 to 30 of SEQ ID NO: 2.

5. The method of claim 1, wherein the method further comprises substituting a glutamine residue at the position corresponding to position 71 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, with a glutamic acid residue.

6. The method of claim 1, wherein the method further comprises substituting a serine residue at the position corresponding to position 193 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, with an arginine residue.

35 7. The method of claim 1, wherein the method further comprises substituting a glutamine residue at the position corresponding to position 242 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, with a serine residue.

40 8. The method of claim 1, wherein the method further comprises substituting an asparagine residue at the position corresponding to position 419 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, with an alanine residue.

45 9. The method of claim 1, wherein the method further comprises substituting an aspartic acid residue at the position corresponding to position 421 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, with an alanine residue.

50 10. The method of claim 1, wherein the method further comprises substituting a tryptophan residue at the position corresponding to position 454 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, with a tyrosine residue.

55 11. The method of claim 1, wherein the method further comprises substituting a tryptophan residue at the position corresponding to position 501 of the amino acid sequence of an alkaline cellulase set forth in SEQ ID NO: 2 or of an amino acid sequence having at least 90% identity with the amino acid sequence of SEQ ID NO: 2, with a tyrosine residue.

\* \* \* \* \*